```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    5, 2004, 10:59:47; Search time 31.6667 Seconds (without alignments) 89.674 Million cell updates/sec
                                                                                                                                                                                                                                                                                       840
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_organelle:*
sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                 US-09-761-636A-10
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL 25:*
                                                                                                                                                                               1 CSVPLTSVC 9
                                                                                       September
                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                       Run on:
```

		Description	Q8gmm5 acinetobact	Q9fxl0 lilium long	Q8jj20 gallus gall	042564 fugu rubrip	Q85562 moloney mur	Q8cg13 mus musculu	Q8kpx4 microcystis	Q849p4 salmonella	Q9y4x6 homo sapien	Q16468 homo sapien	Q81802 zea mays (m	Q9tru7 bos taurus	O35953 mus musculu	Q56140 streptococc	Q9tke5 leptospermu	O9md43 rattus norv
SUMMARIES		ΙD	QBGMM5	Q9FXL0	08JJ20	042564	Q85562	Q8CG13	Q8KPX4	Q849P4	Q9Y4X6	Q16468	Q8L802	Q9TRU7	035953	Q56140	Q9TKES	09MD43
		n DB	2	9 10	7 13	7 13	8 15	9 11	8	8	4	4.	8 10	9	9 11	8	8	8
	* Ouery	Match Length DB	40.0	36.0	34.0	34.0	34.0	34.0	32.0	32.0	32.0	32.0	32.0	32.0	32.0	30.0	30.0	30.0
		Score	20	18	17	17	17	17	16	16	16	16	16	16	16	15	15	15
	Result	No.	г	73	m	4	5	9	7	80	6	10	11	12	13	14	15	16

Query Match 40.0%; Score 20; DB 2; Length 8; Best Local Similarity 80.0%; Pred. No. 1e+06;

1 1 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Plasmid. NON TER SEQUENCE

Q9say7 dioscorea t Q9tkf2 asteromyrtu Q9tkg1 calothamnus P70804 azotobacter Q07624 rous sarcom Q07624 rous sarcom Q07624 rous sarcom Q15890 homo sapien Q15890 pericalymaculu Q15890 pericalymaculu Q15890 pericalymaculu Q15890 pericalymaculu Q15890 pericalymaculu Q15890 pericalyma Q15890 pericalyma Q15890 pericalyma Q15890 azalus gallu Q15810 azalus gallu Q15810 aratus norv Q45615 bacilus su Q15560 escherichia Q15560 escherichia Q15560 escherichia Q15560 escherichia Q15560 pericalymaculuria sa Q15615 homo sapien	SH	8 AA.	ed) sequence update) annotation update)	Gammaproteobacteria; Pseudomonadales; .er.	Z., Gorlenko Z.M.,	sons and possible mechanisms of their EMBL/GenBank/DDBJ databases.	urieva O.	DNA segment	EMBL/GenBank/DDBJ databases. 	IEA.
Р 4 ш м 4 О Г Ф Г Ф М 14	al i gnments		ed) sequence u annotation	геора	in S.Z	and po	nko z	· .>	enBan	DNA;
Q9SAY7 Q9TKF2 Q9TKF2 Q9T8G1 Q9T6G4 Q9T5B9 Q15B9 Q15B9 Q15B9 Q15B9 Q15B9 Q15B9 Q9TAM Q9TU7 Q1069 Q9TU7	ALI	PRT;	Created) Last sec Last and	mmapro	Mindlin	transposons a	Gorlenko		EMBL/G	osomal
0 8 8 2 1 1 1 1 4 4 6 2 4 8 1 1 1 1 1 1 1 1 1 1 2 2 2 2 4 2 2 4 2 2 2 2			23, 23, 24,	, Ga	207;	transpo to the	207;	V.G.	the 1	.1; hrom
80 9 9 7 7 7 9 7 8 8 8 9 9 9 9 9 9 9 9 9 9		PRELIMINARY;	(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.	bacter sp. BW3. pKLH207. a; Proteobacteria; Ga laceae; Acinetobacter xID=106395;	(1) SEQUENCE FROM N.A. STRAIN-BW3; PLASMID-pXLH207; Kholodii G.Y., Yurieva O.V.,	ant tra	ID=p ndli	Petrova M.A., Nikiforov V.G., "A young family of transposable	er genus; 2002) to the CAC80784.1;	CAD31078.1; C:extrachromosomal DNA;
6 6 7 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7		PRELI	(Trev (Trev (Trev (Frag	r sp. 207. oteok e; Ac	M N.A	V.G.; ke aberrant tion."; (OCT-1999)	N N. P	Nik ily o	4Y-20	
0 2 2 4 4 4 E E E E E E E E E E E E E E E			2003 2003 2003 sase	bacter pKLH; a; Pro laceae	E FROM	ov V.G like al nation ed (OC	E FROM	M.A.	ed (M)	J4868 00468
	-	I BGMM5 BGMM5:	01-MAR-2003 01-MAR-2003 01-JUN-2003 Transposase	Tablic to	LI] SEQUENCE FROM STRAIN=BW3; P] Kholodii G.Y.	Nikiforov V.G. "pKLH2-like ab dissemination. Submitted (OCT	[2] SEQUENCE FROM N.A STRAIN=BW3; PLASM Kholodii G.Y., Mi	etrova A youn	ubmitt MBL; A	EMBL; AJ486856; GO; GO:0046821; Plasmid.
11112222222222222222222444444444444444	£	RESULT Q8GMM5 ID Q8	1000EF							
	ĝ p	RE TO A	68444	80000X	R R R R	RR RT	R R R R R R R R R R R R R R R R R R R	RR	Z Z K	¥ 2 2 ¥

Matches

ò

LIMB

```
MEDLINE=97442476; PubMed=9295353; Plummer N.W., McBurney M.W., Meisler M.H.; Plummer N.W., McBurney M.W., Meisler M.H.; Plummer Splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells."; J. Biol. Chem. 272:24008-24015(1997). EMBL; U97673; AAB80916.1; Splicing Co.,0005216; Filon channel activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 4-8 FROM N.A.

MEDLINE=82196891; PubMed=6281735;

Donoghue D.J., Hunter T.;

"A generalized method of subcloning DNA fragments by restriction site reconstruction. Application to sequencing the amino-terminal region of the transforming gene of dazdar murine sarcoma virus.";

Nucleic Acids Res. 10.2549-2564 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDIATE 3305, PubMed=6300424; MEDIATE=83146305; PubMed=6300424; Donoghue D.J., Hunter T.; "Recombination junctions of variants of Moloney murine sarcom virus: Generation and divergence of a mammalian transforming gene."; J. Virol. 45:607-617(1983) . BMBL; K03105; AAA46490.1; ...
                                                                                                                                           Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                 01-0AN-1998 (TrEMBLrel. 05, Created)
01-0AN-1998 (TrEMBLrel. 05, Last sequence update)
01-0IN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.0%; Score 17; DB 15; Length 8; 100.0%; Pred. No. 1e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.0%; Score 17; DB 13; Length 7; Best Local Similarity 71.4%; Pred. No. 1e+06; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moloney murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=11801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA; 732 MW; 98C2D5BEB44DC76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
               7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Truncated env protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŋ
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VPL--VC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSV 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q85562
Q85562;
                                   042564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              985562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Hinomoto;
Udefuji H., Takase H., Hiratsuka K.;
Udefuji H., Takase H., Hiratsuka K.;
"Lilium longiflorum LIM8 gene, promoter region and partial sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, PABOSO987; BABI17856.1; -.
                                                                                                                                                                                                                                                                                                     Lilium longiflorum (Trumpet lily).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Liliales, Liliaceae, Lilium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang Q., Li M.; Li H.; "Cloning and sequencing of 3' UTR of EXFABP gene in chicken."; "Cloning and sequencing of 3' UTR of EXFABP gene in chicken."; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AR1987519; AAL96665.1; -. NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.0%; Score 17; DB 13; Length 7; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.0%; Score 18; DB 10; Length 9; 60.0%; Pred. No. 1e+06; tive 2; Mismatches 0; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-007-2002 (TrEMBLrel. 22, Last annotation update)
Extracellular fatty acid binding protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;
                                                                                                                                                                                                                                                 Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;
;;
                                                                                                                                                                                                                             sequence update)
                                                                                                                                                                       9 AA
Mismatches
                                                                                                                                                                                                         Created)
                                                                                                                                                                       PRT;
                                                                                                                                                                                                                               Last
..
                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
Conservative
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                 LIM8 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SVPLT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                   œ
                                                                         ø
                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=4690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|:|
SMPVT
                                 4 PLTSV
                                                                       PLTQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSV 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSV 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Blood;
 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8JJ20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXFABP.
                                                                                                                                                                                           29FXLO;
                                                                                                                                                                     Q9FXL0
```

Best Loc Matches

à 셤 RESULT 3

1;

Gaps

5;

0

Gaps

·.

RESULT 4

g

à

RESULT 6

```
Markham P.F., Amavisit P., Lightfoot D., Browning G.F.;
"Variation between pathogenic serovars within Salmonella pathogenicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20108806; PubMed=10640831; Midhardt G., Giesler S., Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Schroth A., Bodem J., Royer-Pokora B.; "Genomic structure, alternative transcripts and chromosome location the human LIM domain binding protein gene LDB1."; Cytogenet. Cell Genet. 87:119-124(1999).

EMBL; AJ243097; CAB44408.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                          PipB (Fragment).
Salmonella derby.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.0%; Score 16; DB 4; Length 8; 50.0%; Pred. No. 1e+06; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  32.0%; Score 16; DB 2; Length 8; 40.0%; Pred. No. 1e+06; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          islands.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY144492; AAO49836.1; -.
                                                                    01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Tremblrel. 12, Created)
(Tremblrel. 12, Last sequence update)
(Tremblrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 8 AA; 861 MW; EFC5BDD451A04766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 8 AA; 767 MW; BE6EBDDBB862D5B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q94X6;
01-NOV-1999 (TEMBLrel. 12, Creater
01-NOV-1999 (TEMBLrel. 12, Last st
01-DEC-2001 (TEMBLrel. 19, Last st
Nuclear LIM interactor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=28144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 VPLTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|:|:
1 MPITN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSVP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACP 8
                                                                                                                                                                                                                                                         STRAIN=9813031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q16468
Q16468;
                                                        Q849P4;
                                                                                                                                                                                                                                                                                                                                                                   NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09Y4X6
                                     Q849P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
Q16468
ID Q1646
AC Q1646
DT 01-NO
DT 01-MA
DT 01-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 0
                    Q849P4
                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J;
Wydner K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
"The mouse orthologue of the human ionotropic glutamate receptor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=bloom water sample T96-1;

Baker J.A., Entech B., Neilan B.A., McKay D.B.;

"Monitoring changing toxigenicity of a cyanobacterial bloom using molecular methods.",

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

Bubmit. AN117046; AAM54719.1; -.

NON TER 8 BA, 890 MW; F4DB01A73771A336 CRC64;
                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                         01.MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Glutamate receptor ionotropic N-methyl D-aspartate-like lA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.0%; Score 17; DB 11; Length 9; 50.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.0%; Score 16; DB 2; Length 8; 100.0%; Pred. No. 1e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                              gene (GRINLIA) maps to mouse chromosome 9.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF462417; AA015648.1; -.
EMBL; AF462416; AA015648.1; JOINED.
MGD; MGI:107282; Grinla.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=198099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
9 9
9 AA, 1091 MW; 6A91233EB059C33B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phycocyanin alpha subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Conservative
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microcystis sp. T96-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSVP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 CKLP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 PLT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLT 6
                                                                                                                                                                               (Fragment).
GRINL1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
NON_TER
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8KPX4
```

Matches

RESULT 7

; 0

Matches

ò

οĘ

.. 0

```
(Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                       ω
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||:
1 VPLS 4
  NCBI_TaxID=9913;
                                                                                                                                                                                                       3 VPLTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 VPLT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                         SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           056140
                                                                                                                                                                                                                                                                                          035953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
Q56140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                               035953
  ઠે
                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                   "Walking, cloning and mapping with YACs in 3q27. Localisation of 5 ESTs including 3 members of the Cystatin gene family and dentification of CpG islands."; Gencmics 32:425-430(1996).

EMBL; X88976; CAA61407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GAP-3, GTPase-activating protein (Fragment).
Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                      SEQUENCE FROM N.A.
MEDLINE=96435920; PubMed=8838806;
James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
Anand R.;
            Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Monning S.B., Berdal K.G., Vaitilingom M.M., Holst-Jensen A.;

"Tranformation event-specific quantitative real-time PCR for genetically modified Btl1 maize (Zea mays) and estimation of the impact of exogenous DNA on the limit of quantification.";

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY123624; AAM89275.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.0%; Score 16; DB 10; Length 8; 40.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                 32.0%; Score 16; DB 4; Length 8; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                        SEQUENCE 8 AA; 925 MW; FD5411A7376871E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA; 909 MW; 6046C1B2D77412D7 CRC64;
cosmid cC13-1134 PCR primer 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA.
                                                                                                                                                                                                                                                                                                                                                    8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Conservative
                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLTSV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| :
4 PVTQI 8
                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                              Pat (Fragment).
PAT.
                                                                                                                                                                                                                                                                   4 PLT 6
                                                                                                                                                                                                                                                                                        4 PLT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                 DBLB02;
                                                                                                                                                                                                                                                                                                                                                    Q8L802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9TRU7
                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITIRE=97442476; PubMed=9295353;
Plummer N.W., McBurney M.W., Meisler M.H.;
Plummer N.W., McBurney M.W., Meisler M.H.;
"Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:4008-44015(1997).
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                         The purification of a Rapl GTPase-activating protein from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                          ;
MEDLINE=92112868; PubMed=1309786;
Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
Burgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.0%; Score 16; DB 11; Length 9; 75.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                     Score 16; DB 6; Length 9;
Pred. No. 1e+06;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus thermophilus.

Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus, Streptococcus, NCBI_TaxID=1308;
                                                                                                                                                                                                        89EDA77B47604B5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA; 898 MW; 22D92865B735B737 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:103169; Scn8a.
GO; GO:0007628; P:adult walking behavior; IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                    brain_cytosol.";
J. Biol. Chem. 267:1546-1553(1992)
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.0%;
Matches 3; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 19, STP6 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
                                                                                                                                                                                                        9 AA; 1063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q56140;
01-NOV-1996 (TrEMBLrel.
```

SEQUENCE FROM N.A.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                           STRAIN=STI1;
MEDLINE=95047254; PubMed=7958782;
Constable A., Mollet B.;
"Isolation and characterisation of promoter regions from Streptococcus thermophilus.";
FBMS Microbiol. Lett. 122:85-90(1994).
EMBL; X78210; CAA55045.1; -.
NON TER 8
SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Must. J. Bot. 48:0-0 (2000).
BMBL; AF184650; AAF03860.1; -.
GO; GO:0009507; C:chloroplast; IEA.
Chloroplast.

NON TER 8
SEQÜENCE 8 AA; 876 MW; ECA1B1B764405056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leptospermum erubescens.
Chloroplast.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Myrtaceae; Leptospermum.
NCbl_TaxID=106049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 30.0%; Score 15; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 18+06; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.0%; Score 15; DB 8; Length 8; Best Local Similarity 75.0%; Pred. No. 1e+06; Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., rKI; 8 AA.
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
AtpB (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PLTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SVP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 SVP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
09TKES
AC 09TKE
DT 01-MA
DT 0
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

Search completed: September 5, 2004, 11:05:42 Job time : 32.6667 secs

5 PTTS 8

This Page Blank (uspto)

```
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
```

OM protein - protein search, using sw model

5, 2004, 10:56:37; Search time 37.3333 Seconds September Run on:

(without alignments)
68.114 Million cell updates/sec

US-09-761-636A-10 Title: Perfect score:

1 CSVPLTSVC 9 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

231240 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 9 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A_Geneseq_29Jan04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

		Description	Aau04529 VEGF base	4 Stem	Humar	Abj37356 G-protein				Aaw45666 HBV X 69	Aay46691 Immunogen			lo	Abp54826 Alpha-Ilb	Abp54835 Alpha-IIb		Abr75294 Biologica		Abj04484 HUVEC cel		Aay64300 Cadherin-	_	0 Bone ma	0 Bone	7 Stem	8 Endot
		ID	AAU04529	ABJ04424	ABG34948	ABJ37356	ABJ37436	ABB05266	ADC44660	AAW45666	AAY46691	ABP54842	ADB79677	AAU03756	ABP54826	ABP54835	ABP54823	ABR75294	AAB51972	ABJ04484	AAY48844	AAY64300	AAU03747	ABJ04620	ABJ04630	ABJ04417	ADC44658
		DB	4	5	Ŋ	9	9	Ŋ	7	7	7	ß	۲	4	S	Ŋ	ß	ø	m	S	(1	m	4	Ŋ	Ŋ	Ŋ	7
		Match Length	0	ω	9	7	7	9	σ	0	9	9	7	σ	σ	σ	6	9	7	œ	0	0	6	σ	σ	6	σ
	Query	tch	0.0	4.0	4.0	0.0	0.0	0.0	26.0	4.0	4.0	4.0	2.0	2.0	52.0	2.0	0.2	2.0	0.0	20.0	0.0	0.0	0.0	0.0	50.0	0.0	0.0
۴	ā	Ma	100	74	64	ō	9	ō	Ñ	54	'n	ù	ij	'n	ŝ	Ŋ	Š	Ŋ	Ŋ	Ñ	Ñ	Ŋ	Ñ	Ñ	'n	ī	ĬΩ
		Score	20	37	32	30	30	30	28	27	27	27	26	26	26	26	26	56	25	25	25	25	25	25	25	25	25
,	Result	No.	7	0	m	4	ς.	9	7	80	σ	10	11	12	13	14	15	16	17	8.	13	20	21	22	23	24	25

Synthetic	Synthetic	Synthetic	Synthetic	Human rel	Human MuM	Amino aci	VEGF base	Insulin-1	Peptide d	Cyclic pe	Endostati	Optimised	Human uro	Alpha-IIb	Alpha-IIb				
Ade78117	Ade78037	Ade78097	Ade77841	Aae05003	Aab60620	Aay84175	Aau04530	Aar36888	Aar43632	Aau03758	Aau03731	Aau03770	Aau03739	Aau03760	Abq35053	Abq68159	Ab 04372	Abp54841	Abp54837
7	17	7.	11	33	0.	75	0.	88	12	89	11	0	6	0.	33	6	2	ri.	.7
ADE7811	ADE7803	ADE78097	ADE7784	AAE05003	AAB60620	AAY84175	AAU04530	AAR36888	AAR43632	AAU03758	AAU03733	AAU03770	AAU03739	AAU03760	ABG35053	ABG68159	ABJ0437	ABP5484	ABP54837
7	^	7	7	4	4	m	4	~	7	4	4	4	4	4	S	2	Ŋ	ហ	S
6	6	σ	Ø.	9	9	7	7	Q.	σ	6	σ	თ	σ	σ	9	0	6	6	6
50.0	50.0	50.0	50.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0	48.0
25	25	25	25	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AAU04529 standard; peptide; 9 AA. VEGF based monocyclic peptide 7. (first entry) 26-SEP-2001 AAU04529;

Human, VEGF, vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Synthetic

 .9 /note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond

WO200152875-A1.

26-JUL-2001.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 8-JAN-2001; 2001WO-US001533

(LUDW-) LUDWIG INST CANCER RES

Cendron A; Stacker S, Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

```
peptide loop fragment from an exposed loop of a growth factor protein and vortising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis. neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRASIL; targeting peptide; bacterial infection;
Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;
inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;
viral infection; cardiovascular disease; degenerative disease.
                                                                                                                                                                                                          hormone-related angiogenic dysfunction, diabetes induced necessions became a sequelae, hypertension induced necesscular sequelae, or chronic liver sequelae, hypertension induced necesscular sequelae, or chronic liver in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic with at least one biological activity induced by VEGF. User with a least one biological activity induced by VEGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 4; L 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stem cell (mesenchymal) targeting peptide 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ04424 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001; 2001WO-US028124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #O200220822-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ04424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ04424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential

Arap W, Pasqualini R;

WPI; 2002-404697/43.

Example 5; Page 75; 167pp; English

centrifugation step.

ö

```
The invention comprises a method (BRASIL - Biopanning and Rapid Analysis of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing at target to a phage of display library in a first phase; exposing the first phase to a second phase; and separating the phase exposing the first phase to a second containing unbound phage in a single differential centification step. When compared to conventional cell phages to be separated to step. When compared to conventional cell panning methods, the BRASIL contification increase in recovery of specific phage and a substantial decrease in background. The BRASIL method is useful for identifying targeting peptides. The targeting peptides identified by the method of the invention are useful for treating disease states, such as:

CC diabetes inflammatory arthritis; atherosolerosis; cancer; autoimmune disease; bacterial infection; varial infection; carcer; autoimmune cdegenerative disease. The present amino acid sequence represents a contained of the invention amino acid sequence represents a contained contained and contained and contained contained and contained contained and contained contained and contained and contained and contained contained contained and contained contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel method for identifying disease targeting peptides. The method comprises exposing a sample from an organ, tissue or cell type of interest, to a phage display library and recovering phage bound to the sample (the phage expresses targeting peptides). The peptides identified by the method of the invention may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 5; Length 9;
Pred. No. 1.4e+06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease; arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human bone marrow targeting peptide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 56; Page 207; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG34948 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001; 2001WO-US027702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arap W, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-383050/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSVPVSSSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200220722-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG34948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
ABG34948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                         ò
```

```
Sequence 7 AA;
                                                  16-JAN-2003
                    9
                                  ABJ37356;
                 Query Match
                    Matches
                              RESULT 4
886888888888888888
                       à
                         g
```

```
;
0
                     antiatheroscierotic, antidiabetic, antibacterial and antiviral activities. The methods and composition are useful for identifying targeting peptides and one or more receptors for a targeting peptides. The targeting peptides are used for selective delivery of therapeutic agents, including gene therapy vectors and fusion proteins, to specific organs, tissues, or cell types in subject. The targeting peptide may also be used for treating diseases such as diabetes mellitus, inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodgkin's disease. The present sequence represents a targeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for producing a compound library. The novel method involves reducing a biological target into a group of one or more amino acids required for interaction with a ligand, to generate a model of the biological target, using the model to define a microenvironment in the biological target, using the model to define a microenvironment in the biological target capable of interacting with the microenvironment, and assembling the motifs which interact with the microenvironment, and assembling the motifs to generate a compound library for synthesis. The novel method is useful to produce compound libraries for screening natural ligands such as peptides and proteins or for producing chemical compounds based on drug motifs for screening. This sequence represents a peptide of a G-protein Coupled Receptor (GPCR), which relates to the novel compound library production method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing compound library, by generating biological target model using target sequence information, defining microenvironments interacting with ligand and motifs interacting with microenvironment, and assembling
cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 5; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-protein coupled receptor peptide region #68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stevens AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABJ37356 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 3; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2002; 2002WO-GB003094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-2001; 2001GB-00016570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crossley R, Rose VS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOF-) BIOFOCUS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-221549/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSPPLTRWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003004147-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
```

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method for producing a compound library. The novel method involves reducing a biological target into a group of one or more amino acids required for interaction with a ligand, to generate a model of the biological target, using the model to define a microenvironment in the biological target capable of interacting with the ligand, defining motifs which interact with the microenvironment, and assembling the motifs to generate a compound library for synthesis. The novel method is useful to produce compound libraries for screening natural ligands such as peptides and proteins or for producing chemical compounds based on drug motifs for screening. This sequence represents a peptide of a G-protein Coupled Receptor (GPCR) including Endothelin BT-A receptor, which relates to the novel compound library production method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          model using
eracting with
                                                                                                                                                                                                                                                                                                  Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing compound library, by generating biological target model us target sequence information, defining microenvironments interacting ligand and motifs interacting with microenvironment, and assembling
                                                                                                                                                                                                                                                                     G-protein coupled receptor endothelin ET-A receptor peptide #68.
                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
   Score 30; DB 6; Length 7;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30; DB 6; Length 7;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stevens AP;
                                                                                                                                                                          ABJ37436 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 7; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB05266 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2002; 2002WO-GB003094
                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-2001; 2001GB-00016570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%;
ilarity 83.3%;
Conservative 1
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rose VS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOF-) BIOFOCUS PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-221549/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
5; Conserv
                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSVPLT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention
                                                                1 CSVPLT
                                                                                             CSLPLT
                                                                                                                                                                                                                                                                                                                                                                  WO2003004147-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA;
                                                                                                                                                                                                                                      08-MAY-2003
                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crossley R,
                                                                                                                                                                                                        ABJ37436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB05266
ID ABB0
XX
                                                                                                                                                             ABJ37436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                            g
                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

endothelial cell binding protein; ECBP; anti-tumour; cytostatic; vasotropic; antipsoriatic; dermatological; ophthalmological; antidabetic; antiarthritic; vulnerary; antiulcer; antiniflammatory; antibacterial; gynaecological; anglogenesis.

Endothelial cell binding peptide SEQ ID NO:389.

(first entry)

18-DEC-2003

ADC44660;

ADC44660 standard; peptide; 9 AA

RESULT 7 ADC44660

| :| : || 1 CKMPTSKVC 9

```
The present invention describes a method for screening a ligand library (LL). The method comprises: (a) contacting the LL with an anti-target (AT) to allow the ligands to bind to the AT: (b) separating unbound ligands with a selected target (T) to allow binding of unbound ligands with a selected target (T) to allow binding of unbound ligands with a selected target (T) to allow binding of unbound ligands with a selected target (T) to allow binding of unbound ligands with a selected target (T) to compensate (C); (d) separating (C) from ligands which do not bind (T); and (C) controllypeptides or oligonucleotides. A ligand (I) identified by the nethod can be used in a cleaning therapeutic or personal care application. The method is preferably useful for identified by the method can be used in a cleaning, which involves contacting peptides (C) useful in cleaning compositions, which involves contacting peptides (I) interay with AT such as fabric, ceramic, glass, stainless steel or library with AT such as fabric, ceramic, glass, stainless steel or contacting unbound AT peptides; contacting unbound AT peptides; contacting method as exain, soil-based derived stain, and charted stain, soil-based derived stain, oil-based derived stain, and charted stain, soil-based derived stain, oil-based derived stain, oil-ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening ligand library comprises allowing binding of ligand with antitarget, contacting unbound ligands with selected target to form target-bound ligand complex and identifying target bound ligands on the complex.
                                                                                                                                                                                                                                                                                                                                 Human; tumour necrosis factor alpha; TNF-alpha; VEGF; detergent; stain; bacteriophage; phage library; vascular endothelial growth factor; collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.
                                                                                                                                                                                                                                         Vascular endothelial growth factor binding peptide V-20 SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murray CJ, Tijerina P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 28; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001, 2001WO-US011811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-2000; 2000US-0197259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified bacteriophage.
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMV ) GENENCOR INT INC
                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-139323/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200179479-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                        29-AUG-2003
04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Estell DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-2001
ABB05266;
```

Tsaioun K;

Morris AJ,

Lamphere L,

Gyuris J,

(GPCB-) GPC BIOTECH INC.

01-NOV-2002; 2002WO-US035258 01-NOV-2001; 2001US-0334822P

WO2003037172-A2

Synthetic.

08-MAY-2003.

```
The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell peptide or polypeptide which includes one or more endothelial cell binding protein (BCBP) sequences. A peptide of the invention has anticumous, cytostatic, vasotropic, antipacitatic, dermatological, antidiabetic, antiarthritic, dermatological, antidiabetic, antiarthritic, vulnerary, antiulcer, ophthalmological, antidiatoterial, and gynaecological activity. The peptide cell so promoting, reducing the proliferation and/or migration of cendethelial cells, by treating the cells with an ECBP agonist, which is preferably the peptide, to promote proliferation and/or migration of the created cells with an ECBP antagonist, which is preferably the peptide of the invention. A peptide of the invention is also useful for manufacturing a medicament for promote or reduce anglogenesis at one or more sites in trated mammal. The medicament is useful for promoting or reducing cangiogenesis at one or more sites in anglogenesis. ECBP sequences are useful to alter the infectivity spectrum of invention particle. The present sequence represents an ECBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel synthetic or recombinant polypeptide useful for promoting, reducing proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.0%; Score 28; DB 7; Length 9; 33.3%; Pred. No. 1.4e+06; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; SEQ ID NO 389; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 56.0%;
Best Local Similarity 33.3%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-482072/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDLPTSRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
à
```

· 0

Gaps

..

셤

Query Match 60.0%; Score 30; DB 5; Length 9; Best Local Similarity 44.4%; Pred. No. 1.4e+06; Matches 4; Conservative 2; Mismatches 3; Indels

```
High-A3-like molecules. A cytotoxic T cell (TLD) response against a particular antigen (Ag) is induced in a patient by contacting a CTL with an immunogenic peptide of 9-15 amino acids which binds to at least two High-A3-like molecules with dissociation constant less than 500 nM and induces a cytotoxic T cell response. The immunogenic peptide has a sequence of 9 amino acids, comprising a binding motif, with from the N-to C-termini: primary anchor sites (RRM) at positions 2 (selected from Ala, leu, Ile, Val, Met, Ser or Thy) and 9 (Arg or Lys) and at least one ceronary anchor sites (SAR), i.e. Tyr, Phe or Tro at positions 3, 6 or 7, and/or pro at position 8. The immunogenic peptides are used in peptide based vaccines and therapeutic compositions, for treating viral, based vaccines and therapeutic compositions, for treating viral, constaint or fungal diseases or cancer, e.g. prostatic cancer, hepatitis B or C, renal or cervical carcinoma, lymphoma, cytomegalovirus infection or condyloma acuminatum. They can also be used to elicit a CTL response the nation acuminatum of the cells to the patient, e.g. where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents an immunogenic peptide with binding affinity for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the patient does not respond to peptide vaccines or other therapies. Selection of specific residues for PAR and SAR results in higher binding affinity and thus increased immunogenicity. (Updated on 27-AUG-2003 to
                                                                                                                                                                    HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity; HLA-A3 supermotif; tumour; infection; parasite; CTL; antigen; HIV pol; HBV; hepatitis b virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inducing cytotoxic T cell response against specific antigen - using immunogenic peptide with binding affinity for HLA-A3-like molecules, treat or prevent tumours and infections by virus, parasites etc.
                                                                                                                                   HBV X 69 peptide with binding affinity for HLA-A3-like molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.0%; Score 27; DB 2; I 57.1%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 37; 79pp; English.
AAW45666 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                               97WO-US003778.
                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0013113P
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chestnut RW,
                                                                             (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-470637/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSVPLTS 7
                                                                                                                                                                                                                                                        Synthetic.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CALPFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CYTE-) CYTEL
                                                                                                                                                                                                                                                                                                                                                                                           10-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1996;
                                                                                                                                                                                                                                                                                                               WO9733602-A1
                                                                           27-AUG-2003
09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                        18-SEP-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
ð
```

t

```
AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
having a human major histocompatibility complex (MHC) Class I (also known
as human leukcovyte antigen (HLA) binding motif. The immunogenic peptides
can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
cor A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
the antigen from which the peptide is derived. Cytotoxic T lymphocytes
(CTLS) which destroy antigen-bearing cells are normally induced by an
attigen in the form of a peptide fragment bound to a HLA molecule, rather
than the intact foreign antigen itself, and are particularly important in
cution in the form of a peptide fragment bound to a HLA molecule, rather
therefore useful therapeutically to treat or prevent viral infections and
cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
conditions. They are also useful diagnostically, and can be used to
induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
the peptide e.g. to produce CTLs ex vivo for influsion back into a
cancers. The polynucleotides encoding the immunogenic peptides are also
the peptide e.g. to produce CTLs ex vivo for influsion back into a
cut useful therapeutically and for immunisation as above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                    Immunogenic peptide having a human leukocyte antigen binding motif #1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.0%; Score 27; DB 2; Length 9; 57.1%; Pred. No. 1.4e+06; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 81; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP54842 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sette A, Kubo RT, Sidney J,
                                                                                                                                                                                                                                                                                                                             98WO-US005039.
                                                                                                                                                                                                                                                                                                                                                              98WO-US005039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Query Match
Best Local Similarity 57.10,
                01-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-551214/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSVPLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALPFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9 AA;
                                                                                                                                                                                                                                                   WO9945954-A1.
                                                                                                                                                                                                                                                                                                                           13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                              13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-2003
                                                                                                                                                                                                                                                                                       16-SEP-1999
                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP54842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP54842
à
```

ö

Gaps

٠,

1; Indels Length 9;

Mismatches

5

AAY46691 standard; peptide; 9 AA.

AAY46691

AAY46691 ID AAY XX AC AAY

```
viral infections; non-viral infections; proliferative disease; inflammatory disease; allergic disease; autoimmune disease.
                                                                                                                                                                                                                                                                                                  WPI; 2003-221750/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                  (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLTGMC
                                                                                      WO2003006654-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                      Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                   23-JAN-2003.
                                                                                                                                                                                                                                                   Weber O, Fi
Fleming SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU03756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                  disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU03756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of a novel alpha-IIb beta-3 integrin (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensus binding motif (val-pro-Trp) and was identified by focusing a phage library screening on integrin ligands which are not blocked by a GRGDS peptide. The VPW motif is present in the A3-domain of von Wilebrand factor (vWf), suggesting that vWf is an activator of the alpha-IIb beta-3 complex, enabling stable platelet-VWf interaction. The invention relates to the use of novel peptides (see ABPS4823-25) comprising the consensus binding motif as pharmaceuticals for the treatment of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New alphallb beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue regeneration.
                                                                                                                                                                                      'note= "binding motif, region specifically described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virucide, anti-HIV; hepatotropic, antiinflammatory, cytostatic, vulnerary, antiasthmatic; antiallergic, dermatological, antidiabetic; immunosuppressive; antirheumatic; antiarthritic; thyromimetic; protozoacide; amoebicide; antibacterial; gene therapy; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                      Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 27; DB 5; Length 9; Pred. No. 1.4e+06;
           Alpha-IIb beta-3 integrin activating peptide.
                                                                                                                                                                                                                                                                                                                                                                   (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parapoxvirus ORF 100 C-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 12; 34pp; English.
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB79677 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.0%;
44.4%;
                                                                                                                                                                                                                                                                                                                                      12-MAR-2001; 2001FI-00000492.
                                                                                                                                                                                                                                                                                                      12-MAR-2002; 2002WO-FI000193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Gahmberg CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                       Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDVPWRDLC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-750482/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSVPLTSVC
                                                                                                                                           Key
Disulfide-bond
                                                                                                                                                                                                                                         WO200272619-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Koivunen E,
                                                                                                                                                                                                                                                                         19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB79677;
                                                                                                         Synthetic.
                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB7967
```

```
The invention relates to a novel purified and isolated polymucleotide (S1, (N1) of Parapoxvirus ovis (PPVO) comprising a nucleotide sequence (S1, not defined in the specification), or its complementary sequence, fragment or functional variant. A polymucleotide of the invention has virucide, anti-HIV, hepatotropic, anti-Arbritic, thyrominetic, untindiabetic, contropropersity, anti-Arbritic, thyrominetic, immunosuppressive, anti-Arbritic, thyrominetic, protozoacide, amoebicide, and anti-Arbritic, thyrominetic, protozoacide, amoebicide, and anti-Arbritic, thyrominetic, protozoacide, amoebicide, and anti-Arbritic, thyrominetic, compared and fragments of a provogenome and transportation of anti-Arbritic, thyrominetic, compared and fragments of a provogenome are useful for manufacturing polynucleotides, or recombinant virus scomprissing a Vaccinia virus genome and fragments of a prov genome are useful for manufacturing the papillomatosis, herpes virus infections, liver fibrosis, HIV infections or influences, wayoolsame, amoeba or plasmedia, confictions with mycobacteria, mycoplasma, amoeba or plasmedia), asthma or conditions related to healing of wounds), allergic disease, and/or autoimmune diseases (systemic lupus erythematosus, Sjogren's disease, and/or autoimmune diseases (systemic lupus erythematosus, Sjogren's disease, Hashimoto's thyroiditis, rheumtoid arthitis or diabetes mellitus). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide and recombinant proteins of Parapoxvirus ovis, useful for manufacturing a medicament for treating virus related disease, viral infections, non-viral infections, proliferative disease or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclic; lymphocyte function associated antigen-1; LFA-1; asthma; intracellular adhesion molecule; ICAM-1; inhibitor; leukaemia; haematopoietic neoplastic disease; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·
0
                                                                                                                                                                                                                                                                            Mercer AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyclic peptide inhibitor of LFA-1/ICAM-1 interaction #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.0%; Score 26; DB 7; Length 7; 66.7%; Pred. No. 1.4e+06; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                            Schlapp T,
                                                                                                                                                                                                                                                                                      Siegling A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Page 37; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU03756 standard; peptide; 9 AA
12-JUN-2002; 2002WO-EP006440.
                                                                                         13-JUN-2001; 2001NZ-00512341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                      Friederichs SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
```

ö

ò d

Synthetic.

```
The present sequence is that of a novel alpha-IIb beta-3 integrin (glycoprotein Ilb/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensus binding motiff (Val-Pro-Trp) that was identified by focusing a phage library screening on integrin ligands, which are not blocked by a GRGDS peptide. The motif is present in the A3-domain of von Willebrand factor (VWf), suggesting that vWf is an activator of the alpha-IIb beta-3 complex, enabling stable platelet-VWf interaction. The invention relates to the use of novel peptides
                                                                                                                                                                                                                                                     New alphalib beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising the consensus binding motif as pharmaceuticals for the treatment of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "binding motif, region specifically described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26; DB 5; I
Pred. No. 1.4e+06;
1; Mismatches 4;
                                                                                                                                                    (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-IIb beta-3 integrin activating peptide.
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP54835 standard; peptide; 9 AA.
                                                                 12-MAR-2002; 2002WO-FI000193.
                                                                                                            2001FI-00000492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-2002; 2002WO-FI000193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2001; 2001FI-00000492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                          Gahmberg CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ei ri
                                                                                                                                                                                                                                WPI; 2002-750482/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||
CAVPWARYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200272619-A1
                                                                                                            12-MAR-2001;
                                                                                                                                                                                          Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38-JAN-2003
                           19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP54835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP54835
          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents the amino acid sequence of cyclic peptide inhibitor #33 of lymphocyte function associated antigen-1 and intracellular adhesion molecule (LRA-1/CRM-1) interaction. A composition comprising a cyclic peptide inhibitor of LRA-1/ICRM-1 interaction is useful for treating haematopoietic neoplastic disease, myocardial infarction, radiation injury, asthma, rheumatoid arthritis or lymphoma metastasis. The composition is also useful for inhibiting in a subject the interaction between LRA-1 expressed on a leukocyce and ICRM-1 expressed on another cell, preventing retinoic acid, syndrome in a subject receiving all-trans retinoic acid, inhibiting growth of leukaemia cells, inhibiting emigration of leukocyces from blood into tissue and screening a candidate compound for binding to ICRM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising a cyclic peptide inhibitor of lymphocyte function associated antigen-1 and intracellular adhesion molecule 1 interaction, for treating e.g. asthma and myocardial infarction.

    .5
/note= "binding motif, region specifically described in
Claim 1"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
radiation injury; rheumatoid arthritis; lymphoma metastasis; retinoic acid syndrome; all-trans retinoic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 4; Length 9;
Pred. No. 1.4e+06;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-IIb beta-3 integrin activating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                       (SCTE-) SCI & TECHNOLOGY CORP @UNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 23; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP54826 standard; peptide; 9 AA.
                                                                                                                                                                                      16-JAN-2001; 2001WO-US001382.
                                                                                                                                                                                                                              14-JAN-2000; 2000US-00483550.
16-JAN-2001; 2001US-00760599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALRMRSIC 9
                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-432906/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                     WO200151508-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200272619-A1
                                                                                                                                             19-JUL-2001
```

Synthetic.

Region

cyclic.

ABP54826

ð a

ö

```
The present sequence is that of a novel alpha-IIb beta-3 integrin (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensus binding motif (Val-Pro-Trp) and was identified by focusing a phage library screening on integrin ligands which are not blocked by a GRGDS peptide. The VPW motif is present in the A3 domain of von Willebrand factor (VWF), suggesting that VWF is an activator of the alpha-IIb beta-3 complex, enabling stable platelet-VWF interaction. The invention relates to the use of novel peptides (see for the treatment of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                 New alphallb beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3. .5
/note= "binding motif, region specifically described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 5; Length 9;
Pred. No. 1.4e+06;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "any amino acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "any amino acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "any amino acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-IIb beta-3 integrin activating peptide.
            (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                          Disclosure; Page 12; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP54823 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-2002; 2002WO-FI000193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1"
                                         Gahmberg CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ō.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-750482/81
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200272619-A1
                                                                                                                                              regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JAN-2003
                                         Koivunen E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP54823;
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
ઠે
```

ó

Gaps

```
(glycoprotein InD/III or CP4/CD61) activating peptide. This cyclic peptide comprises a consensus binding motif (val-Pro-Trp) that was identified by focusing a phage library screening on integrin ligands, which are not blocked by a GRGDS peptide. The motif is present in the Adomain of von Willebrand factor (vWf), suggesting that vWf is an activator of the alpha-IID beta-3 complex, enabling stable platelet-vWf interaction. The invention relates to the use of novel peptides comprising the consensus binding motif as pharmaceuticals for the Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                                                                                New alphalib beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                The present sequence is that of a novel alpha-IIb beta-3 integrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 5; Length 9; Pred. No. 1.4e+06;
                                                    (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5, 2004, 11:03:34
                                                                                                                                                                                                                                                             Claim 2; Page 19; 34pp; English.
                 12-MAR-2001; 2001FI-00000492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September
Job time : 38.333 secs
                                                                                         Koivunen E, Gahmberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                            WPI; 2002-750482/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CXVPWXXXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                      regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
g
```

```
Sequence 10, Appl Sequence 24, Appl Sequence 98, Appl Sequence 38, Appl Sequence 34, Appl Sequence 147, App Sequence 480, App Sequence 25, Appl Sequence 25, Appl Sequence 3614, App Sequence 314, App S
                                                                                                                                                                                       September 5, 2004, 11:05:54; Search time 35.667 Seconds (without alignments) 79.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (egn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
(cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.ppp:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-761-636A-10
2 US-00-832-208-24
US-09-832-23-98
4 US-10-303-331-98
4 US-10-286-457-389
US-09-760-599-34
US-10-254-446A-147
US-10-254-446A-147
US-10-601-953-609
US-10-601-953-609
US-10-601-953-609
US-10-601-953-809
US-10-869-3614
US-10-305-393-3614
US-10-395-393-3614
US-10-395-393-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*
                                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                       US-09-761-636A-10
50
1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0
60.0
60.0
60.0
522.0
60.0
60.0
60.0
60.0
60.0
60.0
                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.
```

```
sequence 293, App Sequence 9, Appli Sequence 16, Appli Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 284, Appl Sequence 249, App Sequence 256, App Sequence 778, App
                                                                                                                                                                                                                                 Sequence 256, App
Sequence 257, App
Sequence 778, App
Sequence 792, App
Sequence 1314, App
Sequence 1319, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-09-761-636A-10

i Sequence 10. Application US/09761636A

i Petent No. US20020065218A1

i GENERAL INFORMATION:

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: GENDRON, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

TITLE OF INVENTION VUMBER: US/09/761,636A

CURRENT APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATCHIN VERSION 3.0

SEQ ID NO 10

TENGRAL OF SECTION NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 50; DB 9; Length 9; larity 100.0%; Pred. No. 1.2e+06; Conservative 0; Mismatches 0; Indels
US-10-458-334-2
US-08-344-824-293
US-09-760-599-9
US-09-760-599-17
US-09-760-599-36
US-09-760-599-38
US-09-760-599-38
US-09-760-599-38
US-09-760-599-38
US-09-760-599-38
US-09-760-599-38
US-09-760-599-38
US-09-760-599-38
US-09-935-430-249
US-09-935-430-444
US-10-277-292-349
US-10-280-340-349
US-10-280-340-349
US-10-280-340-349
US-10-280-340-349
US-10-107-532-256
US-10-107-532-256
US-10-107-532-257
US-10-107-532-257
US-10-107-532-257
US-10-107-532-257
US-10-107-532-257
US-10-107-532-257
US-10-107-532-257
US-10-107-532-257
US-10-107-532-31319
US-10-107-532-31319
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-10-363-208-24
; Sequence 24, Application US/10363208
; Publication No. US20040048243A1
   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSVPLTSVC
   US-09-761-636A-10
  444444444444444444444444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
 g
```

```
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
APPLICANT: Board of Regents, The University of Texas System TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting FILE REPERENCE: 005774.P005PCT CURRENT APPLICATION NUMBER: US/10/363,208 NUMBER OF SEQ ID NOS: 273 SOFTWARE: PatentIn version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: peptides screened from a phage display random CTHER INFORMATION: peptide library US-09-832-723-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                               .,
0
                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98, Application US/09832723

Patent No. US20020098524A1

GENERAL INFORMATION:

APPLICANT: Batell, David A.

APPLICANT: Chen, Yiyou

APPLICANT: Murray, Christopher J.

APPLICANT: Tijelna, Pilar

ITILE OF INVENTION: METHODS FOR SELECTIVE TARGETING

FILE REFERENCE: GC617-2

CURRENT APPLICATION NUMBER: US/09/832,723

CURRENT FILING DATE: 2001-04-11

PRIOR PILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 117

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 98

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jamssen, Giselle G. APPLICANT: Murray, Christopher J. APPLICANT: Winetzky, Deborah S. TITLE OF INVENTION METHODS FOR SELECTIVE TARGETING FILE REFERENCE: GC617-3 CURRENT APPLICATION NUMBER: US/10/303,331
                                                                                                                                                                                                                                                                                                                                                                Query Match 64.0%; Score 32; DB 12; L
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.0%; Score 30; DB 9; I 44.4%; Pred. No. 1.2e+06; ative 2; Mismatches 3;
                                                                                                                                                                                                                                                                                    LOCATION: \{1\}..\{9\} OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-303-331-98; Sequence 98, Application US/10303331; Publication No. US20030152976A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CKMPTSKVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSPPLTRWC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSVPLTSVC
                                                                                                                                                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-832-723-98
                                                                                                                                                                                                                                                                                                                              US-10-363-208-24
                                                                                                                                                      SEQ ID NO 24
LENGTH: 9
                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
```

```
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based; OTHER INFORMATION: ability to selectively bind to endothelial cells US-10-286-457-389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 389, Application US/10286457

Publication No. US20030166004A1

GENERAL INFORMATION:

APPLICANT: JENO GYURIS et al.

TILLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY

TILLE OF INVENTION: ENOUTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY

CURRENT APPLICATION NUMBER: US/10/286,457

CURRENT PILING DATE: 2002-11-01

PRIOR APPLICATION NUMBER: 60334822

PRIOR FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 684

SOFTWARE: Patentin version 3.1

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Larson Mr., Richard S.
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction FILE REFERENCE: SCI200/4-1CIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: peptides screened from a phage display random OTHER INFORMATION: peptide library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

56.0%; Score 28; DB 14; Length 9;

Best Local Similarity 33.3%; Pred. No. 1.2e+06;

Matches 3; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.0%; Score 30; DB 14; Length 9; Best Local Similarity 44.4%; Pred. No. 1.2e+06; Matches 4; Conservative 2; Mismatches 3; Indels
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: US 09/832,723
PRIOR FILING DATE: 2001-04-11
PRIOR PILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 98
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09760599 Patent No. US20010034326A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| : :|
1 CDLPTSRIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CKMPTSKVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-286-457-389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-760-599-34
                                                                                                                                                                                                                                                                                                                                                                                US-10-303-331-98
```

g

```
Sequence 481, Application US/10322266
Publication No. US20040115135A1
GENERAL INCRMATION
TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
FILE REFERENCE: NPCIOS67
CURRENT APPLICATION NUMBER: US/10/322,266
NUMBER OF SEQ ID NOS: 797
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                              Sequence 609, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology OF Epithelial
TITLE OF INVENTION: Therapeutic Compounds
TITLE OF INVENTION: UNMERR: 06/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOPTWARE: Patentin version 3.2
SEQ ID NO 609
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 25; DB 16; Length 8; 66.7%; Pred. No. 1.2e+06; Live 1; Mismatches 1; Indels
             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 25; DB 16;
66.7%; Pred. No. 1.2e+06;
iive 1; Mismatches 1;
             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic construct US-10-322-266-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-760-599-25
; Sequence 25, Application US/09760599
             ..
-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
4; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 4; Conserv
                                                   4 PLTSVC 9
                                                                                               1 PVTPVC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PVTPVC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PVTPVC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLTSVC
                                                                                                                                                                                    US-10-601-953-609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-601-953-609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-322-266-481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                     ò
                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                        .<del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                  ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-760-599-34
                                                                                   Score 26; DB 9; Length 9; Pred. No. 1.2e+06; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25; DB 12; Length 8; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.0%; Score 26; DB 14; Length 9; Best Local Similarity 44.4%; Pred. No. 1.2e+06; Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Quay, Steven
APPLICANT: Quay, Steven
APPLICANT: Blaffy, Mohammed Abd
APPLICANT: Grapta, Malini
APPLICANT: de Meireles, Jorge
TITLE OF INVENTION: Compositions and Methods for Enhanced
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Belcher, Angela M
APPLICANT: Smalley, Richard E.
APPLICANT: Ryan, Esther
APPLICANT: Lee, Seung-Wuk
TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
FILE REFERENCE: 119927-1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/254,446A
CURRENT FILING DATE: 2003-02-19
PRIOR PILING DATE: 2003-02-19
PRIOR FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 245
SOFTWARE: Patentin version 3.1
SEQ ID NO 147
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/462,452
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: 60/393,066
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 790
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                Sequence 147, Application US/10254446A Publication No. US20030113714A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 480, Application US/10462452
Publication No. US20040037809A1
GENERAL INFORMATION:
                                                                                 Query Match 52.0%;
Best Local Similarity 33.3%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: artificial sequence
                                                                                                                                                                           1 CSVPLTSVC 9
                                                                                                                                                                                                     |::: |:|
1 CALRMRSIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-462-452-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKLQLTNQC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   RESULT 7
US-10-254-446A-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-254-446A-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-462-452-480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
FEATURE:
```

g

```
US-10-395-032-3614
i. Sequence 3614, Application US/10395032
i. Publication No. US20030229199A1
i. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 11, Application US/09761636A; Patent No. US20020065218A1; GENERAL INFORMATION:
SOFTWARE: Patentin version 3.1
SEQ ID NO 387
LENGTH: 9
                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                  Query Match
Best Local Similarity 44.*
Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTFHIDSVC 9
                                                                                                                                                                                                                                                                                                                                                     1 CPDPTTRLC 9
                                                                                                                                                                                                                                                                                                          1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSVPLTSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-395-032-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-761-636A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 3614
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-LC-200-30-20.
Sequence 387, Application US/10286457
Sequence 387, Application US US20030166004A1
GENERAL INFORMATION:
APPLICANT: JENO GYVELS et al.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REPRENENCE: GFOL-P01-178
CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT FILING DATE: 2002-11-01
FRIOR APPLICATION NUMBER: 60/334822
FRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-006-869-3614
US-10-006-869-3614
US-10-006-869-3614

| Sequence 3614, Application US/10006869
| Publication No. US20030082166A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. APPLICANT: Symonds, James Matthew
| APPLICANT: Gour, Barbara J. TITLE OF INVENTION: CADHERIN WEITHOW FUNCTIONS
| TITLE OF INVENTION: CADHERIN WEDIATED FUNCTIONS
| FILE REFERENCE: 100086.407C7 | CURRENT FILING DATE: 2001-12-03 | NUMBER OF SEQ ID NOS: 4052 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NO 3614 | LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                               GENERAL INFORMATION:
APPLICANT: Larson Mr., Richard S.
APPLICANT: Larson Mr., Richard S.
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
FILE REFERENCE: SCI200/4-1CIP
CURRENT PEPLICATION NUMBER: US/09/760,599
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 25
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-760-599-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 25; DB 14; Length 9; 44.4%; Pred. No. 1.2e+06; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 25; DB 9; Length 9; 33.3%; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.4.
                                                                                                                                                                                                                                                                                                                                                                                                                             3; Conservative
             Patent No. US20010034326A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTFHIDSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : : |:|
1 CMLRMNSIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-006-869-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-286-457-387
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
0
                                                                                                              0; Gaps
                                                                           Query Match 48.0%; Score 24; DB 9; Length 7; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-11
                                                                                                                                      3 VPLTS 7 | | | | | | | 2 VPLTS 6
                                                                                                                                        ŏ
```

Search completed: September 5, 2004, 11:16:00 Job time : 36.6667 secs

qq

This Page Blank (uspto)

Н

```
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
APPLICANT: Raolate, Dentata
APPLICANT: Raolate, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
TITLE OF INVENTION: Membrane Dipeptidase
TITLE OF INVENTION: Membrane Dipeptidase
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 09/042,107
NUMBER OF SEQ ID NOS: 452
SOFTWARE: PATENT OF SEQ ID NOS: 452
SOFTWARE: PATENT OF SEQ ID NOS: 452
SEC ID NO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34, Appl Sequence 199, App Sequence 199, App Sequence 3614, App Sequence 25, Appl Sequence 25, Appl Sequence 21, Appl Sequence 21, Appl Sequence 30, Appl Patent No. 5190920 Patent No. 5506208 Sequence 43, Appl Sequence 43, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (without alignments)
38.719 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, 75
Sequence 36, A
Sequence 38, A
Sequence 9, Ap
Sequence 17, A
Sequence 13, A
Sequence 13, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
                                                                          5, 2004, 11:01:38; Search time 12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*

(Cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

(Cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

(Cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

(Cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

(Cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

(Cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

(Cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-760-599-34
US-09-258-754-199
US-09-042-107-199
US-09-187-859-3614
US-09-839-542B-3614
US-09-722-250D-199
US-09-483-550B-25
US-08-476-134A-21
US-08-476-134A-21
US-08-476-134A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-958-903A-43
US-08-462-018-43
US-08-823-245-43
US-08-823-245-43
US-08-823-245-43
US-08-65-430-49
US-07-963-232A-43
US-09-760-599-17
US-09-760-599-18
US-09-760-599-38
US-09-760-599-48
US-09-760-599-48
US-09-760-599-48
US-09-483-550B-9
US-09-483-550B-9
US-09-483-550B-17
                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-475-955-67
                                                                                                                                                                                                                      389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                        US-09-761-636A-10
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
                                                                                                                                                      1 CSVPLTSVC 9
                                                                          September
                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.64.60
                                                                                                                                       Perfect score:
                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                      Sequence:
                                                                                                                                                                                                                    Searched:
                                                                         Run on:
                                                                                                                           ritle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
```

Sequence 4, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 146, App	122, A 146, 308,	
US-08-195-075-4 US-08-467-083-3 US-08-414-417B-3 US-08-416-48A-3 US-08-496-48A-3	2 US-08-458-3 US-08-458-34-80 US-08-46-80B-3 US-09-258-754-146 US-09-258-754-308	US-09-139-802-92 US-08-660-092-122 US-09-042-107-146 US-09-042-107-308 US-09-042-107-308	US-09-659-786-92 US-08-403-459-25 US-08-926-914-92 US-09-722-250D-146
ннни.	4 CM CM CM	ωωωω 44	4444
00000	0000	00000	0000
46.0 46.0 46.0	46.0 46.0 46.0	46.0 46.0 46.0 46.0	46.0 46.0 46.0
2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	33333	######################################	2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
2 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1 W W W W 1 W 44 TV PO	33 33 34 40 41	2444 2444 45

ALIGNMENTS

```
Gaps
                 Sequence 34, Application US/09760599
Patent No. 663047
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
FILE REFERENCE: SCI200/4-ICIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 34
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-760-599-34
                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 26; DB 4; Length 9; 33.3%; Pred. No. 3e+05; Live 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 199, Application US/09258754 Patent No. 6174687 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 33.3
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CALRMRSIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-258-754-199
US-09-760-599-34
                                                                                                                                                                                                                                                                                                                               FEATURE
```

```
TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 44.4
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSAYTTSPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |: : |||
CTFHIDSVC 9
|: : |||
1 CTFHIDSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                           RESULT 5
US-09-839-542B-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-722-250D-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                      0
                                                                                                                                                                                                                                                                                                           Sequence 199, Application US/09042107
; Sequence 199, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICAMT: Reusalanti, Erkki
; APPLICAMT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; TITLE OF INVENTION: Tissues
; TITLE OF INVENTION: Tissues
; TITLE OF INVENTION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INC. 93-10-10.

GENERAL INC. 93-10-10.

APPLICANT: Blaschuk, Orest W.

APPLICANT: GOUY, BATABARA J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086 407C1

CURRENT APPLICATION NUMBER: U$/09/187,859A

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 3614

LENGTH: 9
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-199
                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 50.0%; Score 25; DB 4; Length 9; Best Local Similarity 44.4%; Pred. No. 3e+05; Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                        4; Indels
                                                                                             Score 25; DB 3; Length 9;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 3;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3614, Application US/09187859A
Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0%;
Best Local Similarity 55.6%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                   50.0%;
                                                                                                   Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSAYTTSPC 9
                                                                                                                                                                                      1 CSVPLTSVC 9
                                                                                                                                                                                                                             1 CSAYTTSPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-187-859-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-187-859-3614
                                                                                                                                                                                                                                                                                                               US-09-042-107-199
                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                               g
                                                                                                                                                                                          ò
```

1 CSVPLTSVC

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 199, Application US/09722250D

Sequence 199, Application US/09722250D

Patent No. 6610651.

Patent No. 6610651.

APPLICANT: Rucelahti, Erkki

APPLICANT: Pasqualini, Renata

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: 2000-11-22

CURRENT APPLICATION NUMBER: US/09/722,250D

CURRENT APPLICATION NUMBER: US 09/042,107

PRIOR PLING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 437

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 199
Sequence 3614, Application US/09839542B
; Sequence 3614, Application US/09839542B
; Patent No. 6569996
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: CAMPGINDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CAMPGINATED FUNCTIONS
; FILE REFERENCE: 100086.40701
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion CHER INFORMATION: recognition sequence US-09-839-542B-3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-722-250D-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 25; DB 4; 55.6%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-760-599-25
```

```
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSVP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-483-434A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-476-134A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                        APPLICANT: Larson Mr., Richard S.
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction FILE REFERENCE: SCI200/4-1CIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT FILING DATE: 2011-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Larson Mr., Richard S.
TITLE OF INVENTION:
PEDIGÉ INHIBITION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
SCHEAT APPLICATION NUMBER: US/09/483,550B
CURRENT FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 25
LENGTH: 9
                                                                                                                                                                                                                                                                          FEATURE:

CTHER INFORMATION: Description of Artificial Sequence:Synthetic

US-09-760-599-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-483-550B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: EVAL, Jacob
APPLICANT: EVAL, Jacob
APPLICANT: TUSZNSKI, Jacob
APPLICANT: TUSZNSKI, Jacob
APPLICANT: TUSZNSKI, George R.
TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
TITLE OF INVENTION: Therapeutic Use Thereof
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                              h Score 25; DB 4; Length 9; Similarity 33.3%; Pred. No. 3e+05; 3; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/09483550B Patent No. 6649592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08483434A, Patent No. 5648461, GENERAL INFORMATION:
Sequence 25, Application US/09760599 Patent No. 6630447
                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : : |:|
1 CMLRMNSIC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1601 Marke
CITY: Philadelphia
STATE: Pennsylvani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : |:|
CMLRMNSIC 9
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-09-483-550B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-483-434A-21
                                                                                                                                                                                               SEQ ID NO 25
LENGIH: 9
                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
```

```
MEDIUM TYPE: Floatey disk.

ONNEUTES: TRAIN TYPE: Floatey disk.

FLUNG DATE: 0'-104-1954

PELING DATE: 2'-104-1954

PELING DATE: 2'-104-1964

PERING PELING DATE: 3'-104-1964

PERING PELING PELING DATE: 3'-104-1964

PERING PELING DATE: 3'-104-1964

PERING PELING DATE: 3'-104-196
```

```
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCTPAKSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
STREET: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-958-903A-43
                                                         RESULT 13
US-07-958-903A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: analog of thrombospondin
                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEORGE P.
TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
THROMEOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
NUMBER OF SEQUENCES: 45
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,181
FILING DATE: 22-NAR-1995
FILING DATE: 02-NAR-1993
APPLICATION NUMBER: 131,565
FILING DATE: 09-CUT-1993
APPLICATION NUMBER: 895,764
FILING DATE: 09-UN-1992
FILING DATE: 09-UN-1992
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 100.0%; Score 24; DB 6; Length 6; ilarity 100.0%; Pred. No. 3e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 48.0%; Score 24; DB 6; Length 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,197
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Patent No. 5190920
; APPLICANT: BYAL, JACOB;HAMILTON, BRUCE K.;TUSZXNASKI,
;GEORGE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5506208-28
;Patent No. 5506208
; APPLICANT: EYAL, JACOB;HAMILTON, BRUCE K.;TUSZYNSKI,
                                                                                                                                                                                                                                             Query Match
48.0%; Score 24; DB 3;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0
      PRIOR FILING DATE: 1993-03-01
                                                                                                             TYPE: PRT ORGANISM: Artificial Seguence
                   NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                       1 CSVP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;SEQ ID NO:28:
; LENGTH: 6
5506208-28
                                                                                                                                                                                                                 US-08-476-134A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:26:
                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5190920-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5190920-26
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lewis, Michael E.
APPLICANT: Smith, Kevin R.
APPLICANT: Callison, Kathleen V.
APPLICANT: Callison, Kathleen V.
APPLICANT: Baldino, Frank
APPLICANT: Idpal, Mohamed
TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 24; DB 1; Length 9; 44.4%; Pred. No. 3e+05; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CUNTRY: Massachusetts
COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/958,903A
FILING DATE: October 7, 1992
CLASSIFICATION NUMBER: 07/361,595
FILING DATE: June 5, 1989
APPLICATION NUMBER: 07/534,139
FILING DATE: June 5, 1989
APPLICATION NUMBER: 07/534,139
FILING DATE: June 5, 1989
APPLICATION NUMBER: 07/534,139
FILING DATE: June 5, 1990
APPLICATION NUMBER: 07/869,913
FILING DATE: April 15, 1992
ATROMEY AGENT INFORMATION:
ANAME: ABENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 02655/003004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-462-018-43; Application US/08462018; Sequence 43; Application US/08462018; Patent No. 2703045; GENERAL INFORMATION: APPLICANT: Lewis, Michael E.
; Sequence 43, Application US/07958903A; Patent No. 5652214
                                                                                                                                                                                                                                                                                                                                                                               E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (617) 542-5070
(617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSVPLTSVC 9
```

0

ð

us-09-761-636a-10.closed.rai

```
5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.0%; Score 24; DB 1;
44.4%; Pred. No. 3e+05;
Live 0; Mismatches
      TITLE OF INVENTION: APPLICATION
TITLE OF INVENTION: PACTORS AND
TITLE OF INVENTION: PACTORS
CORRESPONDENCE ADDRESS:
ADDRESSER: Sish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STREET: 226 Franklin Street
CITY: Boston
STREET: 226 Franklin Street
COUNTRY: U.S.A.
ZIP: MASSACHUSELTS
COUNTRY: U.S.A.
ZIP: O2110-2804
COMPUTER: BASA PALE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: SSA
                   APPLICATION
OF INSULIN-LIKE GROWTH
FACTORS AND
ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: September 5, 2004, 11:07:05
Job time: 13 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 20154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCTPAKSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-823-245-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·,
                                         APPLICANT: Callison, Kathleen V. APPLICANT: Baldino, Frank APPLICANT: Baldino, Frank APPLICANT: Neff, Nicola APPLICANT: Neff, Nicola APPLICANT: IGDAL, MODARMED TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION TITLE OF INVENTION: ANALOGS NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
48.0%; Score 24; DB 1;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY MASSACINSELES
COUNTRY MASSACINSELES
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TREATING DISORDERS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02655/003005
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
CLOCKER: 7, 1992
APPLICATION NUMBER: 07/961,595
FILING DATE: 07/861,595
FILING DATE: 07/84,139
FILING DATE: 07/84,139
FILING DATE: 07/869,913
FILING DATE: 07/869,913
FILING DATE: DATA: 07/869,913
FILING DATE: APPLICATION NUMBER: 07/869,913
FILING DATE: APRIL 15, 1992
APPRICATION NUMBER: 07/869,913
FILING DATE: APRIL 15, 1992
ATORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 02655/00:
TELEPOMUNICATION INFORMATION:
TELEPOMUNICATION INFORMATION:
TELEPRAKE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application US/08823245
Patent No. 5776897
GENERAL INFORMATION:
APPLICANT: Lewis, Michael
APPLICANT: Smith, Kevin R.
APPLICANT: Smith, Kevin R.
APPLICANT: Smith, Kevin R.
APPLICANT: Baldino, Frank
APPLICANT: Neff, Nicola
APPLICANT: Neff, Nicola
APPLICANT: Igbal, Mohamed
ITILE OF INVENTION: TREATING DISORD
Kauer, James C.
Smith, Kevin R.
Callison, Kathleen V.
Baldino, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 20154
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CSVPLTSVC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCTPAKSEC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-462-018-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-823-245-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ó

Gaps

This Page Blank (uspto)

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September Run on:

5, 2004, 11:14:14 ; Search time 21 Seconds (without alignments) 32.064 Million cell updates/sec

US-09-761-636A-11

1 CVPLTSC 7 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues

457

seg length: 0 seg length: 7 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

glycogen phosphory laminin B1 - weste seed protein ws-5 dihydrofolate redu R-phycoerythrin ga Y protein - human catch-relaxing pep tryptophyllin, bas glycoprotein compo MHC H2-L antigen -R-phycoerythrin al acetylcholinestera major protein anti aggrecan - bovine R-phycoerythrin be MHC H2-K-k cell su hypothetical prote schwannomin - mous mabinlin II chain ribulose-bisphosph myomodulin - Calif tyrosine-melanocyt vicilin 57K chain virotoxin - destro R-phycoerythrin al metallothionein-A lg kappa chain V-I hypothetical L2 pr DNA topoisomerase SUMMARIES B34818 A34026 I67345 S08606 A32039 I54357 A60521 F22565 I37263 ECMUCR 65546 S42620 C22565 I49421 E61491 I48105 I48086 A61081 S38516 8090 26992 T0087 Ouery Match Length I Result No.

Ig mu chain V regipallidipin - assas cadmium-binding peacid proteinase liactin I - malaria hemoglobin, extrac phosphoprotein, bo 34.5K structural p 34.5K structural p 35K structural p 35K structural p 10popeptide WS1279 andiotensin-conver dihydrofolate redu contraction-inhibi
2 S43959 2 A55238 2 A39622 2 B45525 2 S6726 2 S1127 2 F44817 2 D44817 2 A61049 2 JU0355 2 A31263 2 A27696
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
ш ш ш ш ш ш ш ш ш ш ш ш ш ш ш ш ш ш ш

ALIGNMENTS

Fighycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment) Cispecies: Gastroclonium coulteri Salasesion: B2566 Biscon: B2566 ANN.

J. Biol. Cham. 260, 4856 4863, 1985

A;Fille: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22565; MUID: 85182601; PMID: 3886644

A;Molecule type: protein

A;Residues: 1-5 < KLO>

.; 47.6%; Score 20; DB 2; Length 5; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels 3; Conservative Query Match Best Local Similarity Matches 3; Conserva

..

Gaps

1 CVP 3

à

Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr. Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr. G.Species: Box primigenius taurus (cattle)
C.Spate: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C.Accession: H48394
R.Mather, I.H.; Banghart, L.R.; Lane, W.S.
Blocchem. Mol. Biol. Int. 29, 545-554, 1993
A.Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
A.Title: A8394; MUD:93250576; PMID:8485470
A.Status: preliminary
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-6 cMAT>

A Experimental source: milk A NOE: sequence extracted from NCBI backbone (NCBIP:131518)

C; Keywords: glycoprotein

h Similarity 50.0%; Pred. No. 2.8e+05; 3; Conservative 0; Mismatches 3; Indels Best Local Similarity Query Match Matches

ô

Gaps

0;

2 VPLTSC 7 1 VELLGC

ö

Gaps

ò g

```
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274; Miker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect: Immun. 59, 312-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: B60274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R-phycocrythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
R-phycocrythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: C22565
R;Klotz, A.V.; Glase. A.N.
A;Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Accession: C22565
A;Molecule type: protein
A;Residues: 1-6 <KLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gispecian - bovine (fragment)

Gispecias: Bos primigenius taurus (cattle)

Gispecias: Bos primigenius taurus (cattle)

Cispecias: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

Cispecias: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998

Cispecias: 14. Saccasion: 842620

Airitle: Aggrecan in bovine tendon.

Airitle: Aggrecan in bovine tendon.

Airitle: Aggrecan in bovine tendon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%; Score 12; DB 2; Length 6; 25.0%; Pred. No. 2.8e+05; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
                                                                                                                                                                                                                                                                                                                                                                                              Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.0%; Score 13; DB 2; 1
50.0%; Pred. No. 2.8e+05;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                           33.3%; Score 14; DB 2; I
66.7%; Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-7 <VOG>
A;Experimental source: flexor tendon
C;Keywords: cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: |
2 PIVS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PLTS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|
PIT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PLT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S42620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
S42620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
167345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C,Accession: A34026
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.; T
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.; T
Biol. Chem. 263, 1140-1145; PS180
A;Title: Divergence in primary structure between the molecular forms of acetylcholineste
A;Reference number: A34026; MUID:88087239; PMID:3335534
         MHC HO-L antigen - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C;Accession: 165546

A;Reference number: 152778; MUID:86106202; PMID:3510743

A;Accession: 15546

A;Accession: 165546

A;Accession: 165546

A;Accession: 165546

A;Reference number: 152778; MUID:86106202; PMID:3510743

A;Accession: 165546

A;Reference number: 152778; MUID:86106503; PMID:3510743

A;Reference number: 152778; MUID:86106503; PMID:3510743

A;Reference number: 16546

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residus: 1-6 KRES-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acetylcholinesterase (BC 3.1.1.7) 5.6S form - Pacific electric ray (fragment) C;Species: Torpedo californica (Pacific electric ray)
C;Species: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lordin 57K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Species: Cajanus cajan (pigeon pea)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-7u1-1990 #sequence_revision 13-Ju1-1990 #text_change 30-Sep-1993
C;Accession: B3418
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
B;Ochem, B;Ophys. Res. Commun. 166, 1446-1452, 1990
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A;Reference number: A34818; MUID:90165956; PMID:2306256
A;Accession: B34818
A;Actuals preliminary
A;Molecule type: protein
A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.7%; Score 15; DB 2; Length 7; 66.7%; Pred. No. 2.8e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15; DB 2; Length 7; Pred. No. 2.8e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: A34026
A,Molecule type: protein
A,Residues: 1-7 (GIBs)
C,Keywords: alternative splicing; carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 35.7
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TTC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VPLT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VPCT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

ò 윱

ö

0

Gaps

RESULT

ò

00

Matches

ð d ö

```
A;Accession: A60521
A;Molecule type: protein
A;Molecule type: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: 149421
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082; PMID:8043949
A;Accession: 149421
                                                                                                                                                                                                                                                                                                             Cyacession: 154377 meduance_revision vz.Aug-1996 #text_cnange Us-NOV-1999
Cyacession: 154377 mechiporuk, T.; Pulst, S.
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are A;Reference number: 154357; MUID:95072570; PMID:7981675
A;Acession: 154357
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ", bacession: A6051]
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95. 295-301, 1990
A;Tile: Purification and characterization of glycogen phosphorylase B from skeletal A;Reference number: A60521; MUID:90227907; PMID:2109669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment) N;Alternate names: glycogen phosphorylase b C;Species: Liza ramada C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
                                                                                                                                                                                                                                schwannomin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: Î-4 <RES>
A;Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.2%; Score 11; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 26.2%; Score 11; DB 2; Length Local Similarity 100.0%; Pred. No. 2.8e+05; nes 2; Conservative 0; Mismatches 0; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         laminin B1 - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 2; Conserv
                                                               4
                                                                                                             m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                      Z=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VP
                                                            m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: NF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A60521
                                                      ð
                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: 80866
R,Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
A;Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes
A;Reference number: 807192; MUID:86247578; PMID:3755102
WHC H2-K-k cell surface glycoprotein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 167345
R;Archbald, A.L.; Thompson, N.A.; Kvist, S.
ENBO J. 5, 957-965, 1986
A;Title: A single nucleotide difference at the 3' end of an intron causes differential A;Reference number: 153243; MUID:86247587; PMID:3013627
A;Accession: 167345
A;Accession: 167345
A;Accession: Logar and a single from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-6 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Horvath, A.; Kastin, A.J.
N. Biol. Chem. 264, 2175-2179, 1989
A;Title: Isolation of tyrosine-melancoyte-stimulating hormone release-inhibiting factor
A;Reference number: A32039; MUID:89123285; PMID:2563371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 2 estrogen receptor 5'-region - chicken
C'Species: Gallus gallus (chicken)
C'Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Bos primigenius taurus (cattle)
C,Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27432.1; PID:g584490
C;Superfamily: unassigned leader peptides
                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458 C;Genetics: A;Introns: GB:A;Introns: GB:C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 2; Length 6; Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 12; DB 2; Length 7;
Pred. No. 2.8e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.2%; Score 11; DB 2; Le
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Experimental source: brain C. Superfamily: unassigned animal peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%;
Matches 2; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.6%;
ilarity 50.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translation not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-4 < HOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-7 < KRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPDC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LAHC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A32039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: A32039
```

d 8

mus

```
Geed protein ws-5 - winged bean (fragment)
C;Species: Psophocarpus terragonolobus (winged bean)
C;Species: Psophocarpus terragonolobus (winged bean)
C;Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 07-0ct-1994
C;Accession: E61491
R;Hirano, H.
A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dim A;Reference number: A61491; MUID:89351606; PMID:2765119
A;Accession: E61491
A;Accession: E61491
A;Accession: E61491
A;Accession: E61491
C;Keywords: graphinary
A;Molecule type: protein
A;Residues: 1-7 <HIR>
C;Keywords: glycoprotein; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                      .
0
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                        Gaps
                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                 Query Match
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                        5 TSC 7
::|
3 STC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VP 3
                                                                                                                                                                                                                                                                                                      RESULT 15
E61491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                            g
                                                                                                                                                                                à
```

Search completed: September 5, 2004, 11:19:01 Job time: 22 secs

3 VP 4

*

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

5, 2004, 11:07:09; Search time 16 Seconds (without alignments) 22.781 Million cell updates/sec September Run on:

US-09-761-636A-11 1 CVPLTSC 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Daylor litroria	hernes	2984 lenting		0420	litoria	litoria	00	mytilus	ᆵ	citro				P81675 pinus pinas	Sus so	psen		, ,	bothr	P82100 litoria rub	_		P42985 leptinotars		-	P81807 carcinus ma	P81808 carcinus ma	P20104 enterococcu	17			1875 panagrell
SUMMARIES	ID	EIO1 LITRU		MNP1_LEPDE	TPFY PACDA	CARP MYTED	TY51_LITRU	EI03_LITRU	CIP1_MYTED	CIP2_MYTED		BIOA_CITFR	PRCT_PERAM	TRPI_PSEPU	CIA_ENTFA	UNO6_PINPS	THYL PIG	DCML_PSECH	RM01 YEAST	TUFT HUMAN	BPP7 BOTIN	1 1		SUGA_ACHDO	. –	- 1	ALL3_CARMA	- 1			CHOX_ALCSP		FAR1 HELTI	FAR4_PANRE
	Length DB	6 1	9		7 1		7 1							6 1								5 1				9								
ф	Query Match Length	31.0	26.2		9	3	23.8	21.4	÷	ы	п.	σ,	ou .	19.0	3	g)	9	9	9	9	16.7	9	9	16.7	י פ	16.7	9 (16.7	16.7	16.7	16.7	٠	16.7	
	Score	13	11	11	11	10	10	σ	σ.	σ,	σ,	σ (3 0	Φ (20	&	7	7	7	7	7	Ĺ	7		~ (- 1	۱ -	~ (- 1		7	7	7	7
	Result No.		7	m	4	S,	φ.	7	œ (٠ ب	01	11	12	13	† †	15	16	17	18	19	20	21	77	23	7 0	2 7	10	7 0	20 00	N 6	30	7 7	3.2	33

P41866 calliphora P99025 mus musculu P36960 carnobacter P38642 mus musculu P81351 clostridium P80630 zea mays (m P12997 citrobacter P58261 daucus caro P82072 litoria rub P82073 litoria rub P41491 locusta mig P06294 dactylium d
FARB CALVO GFRP MOUSE LANC CARUI UF04 MOUSE UNO6 CLOPA UC24 MAIZE B108 CITFR PSK DAUCA RE31 LITRU RE32 LITRU LOKI LOCMI
<u> </u>
16.7 16.7 16.7 11.9 11.9 11.9 11.9
<u> </u>
шшшшшш чччч чшпгшшчччч

ALIGNMENTS

ð 셤

```
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA; 831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                   2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A29342; ECMUCR.
Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                 NCBI_TaxID=75988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 VPL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 MPM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                              2 VP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARP MYTED
                                                                                                                                                                                                                                                                                                                   MOD RES
MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P10420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARP_MYTED
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
  expression of ULJ8, a true late gene involved in capsid assembly."; J. Virol, 65:769-786(1991).
-!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S., Grauwels L., van Leuven F., de Loof A.; Identification, characterization, and immunological localization a novel myotropic neuropeptide in the Colorado potato beetle, Leptinotarsa decembineata.";

Peptides 16:365-374 (1995).

--- FUNCTION: Myotropic peptide. Stimulates the contractions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annoctation update)
Myotropic neuropeptide 1 (Led-WNP-1)
Leptinoctarsa decemlineata (Colorado potato beetle).
Enkaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota,
Neoptera; Endopterygota, Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
Chrysomelini; Leptinotarsa.
                                                          -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.2%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                          Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD RES 7 7 AMIDATION.
SEQÜENCE 7 AA; 705 MM; 6DD73768745B5DB0 CRC64;
                                                                                                                                                                                                                                 6 AA; 703 MW; 67376451A336F000 CRC64;
                                                                                                                                                                                                                                                         DB 1; Le
1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 41, Created)
(Rel. 41, Last sequence update)
                                                                                                                                                                                                      Capsid assembly; Coat protein; DNA-binding.
                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                      26.2%; Score 11;
ilarity 100.0%; Pred. No.
Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95380343; PubMed=7651886;
                                                                                                                                                                                            EMBL; M57646; AAA45830.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                     Local Similarity
nes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PL 4
                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                3 PL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P83455;
28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                          ΡΓ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PACDA
                                                                                                                                                                                                                                                                                                                                                                                                         MNP1 LEPDE
P42984;
                                                                                                                                                                                                                        NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
TPFY PACDA
ID TPFY_Pi
                                                                                                                                                                                                                                                                                                                                                                                           MNP1_LEPDE
                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                             QQ
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . , NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                           SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brain Res. 422:374-376(1987).
-!- FUNCTION: This peptide exhibits both potentiating (contraction)
and inhibitory (relaxation) effects on the anterior byssus
retractor muscle.
                                                                                                                                                                                                                                                         TISSUE-Skin secretion;
Chen T.B., Orr D.F., Shaw C.;
"Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural
characterization, pharmacological activity and cloning of precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytloidae; Mytilidae; Mytilidae; Mytilus.
Tryptophyllin-1 (PdT-1).
Pachymedusa dacnicolor (Giant mexican leaf frog).
Patharyota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Phyllomedusinae; Pachymedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                 smooth muscle.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
-!- MASS SPECIFOMETRY: MW-809.2; METHOD=MALDI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0045986; P:negative regulation of smooth muscle contra.
Amphibian defense peptide; Amidation; Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88052022; PubMed-3676797;
Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
Muneoka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
Brain Res. 422:374-376(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.2%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 7 AMIDATION.
7 AA; 794 MW; 7772D37DC7776350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION.
6734072687669DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 1; I
Pred. No. 1.4e+05;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
01-ART-1989 (Rel. 10, Last annotation update)
Mytilus edulis (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. NO. +...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                    cDNA.";
Submitted (SEP-2002) to Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.8%;
ilarity 33.3%;
Conservative
```

· 0

ð

Sun Sep

us-09-761-636a-11.closed.rsp

```
TISSUE-Pedal ganglion;
MEDLINE=88340357; PubMed=3377776;
Hirata T., Kubota I., Twaswa N., Takabatake I., Ikeda T., Muneoka Y.;
Structures and actions of Mytlius inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
-: FUNCTION: Inhibitory action on contractions in several molluscan
                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide I (MIP I).
Mytilus edulis (Blue mussel).
Eukaryota, Metazoa, Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytillidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.4%; Score 9; DB 1; Length 6; 50.0%; Pred. No. 1.4e+05; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 AA; 637 MW; 72C9C68775B81000 CRC64;
                                                                                                                                                                                                   6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.00,
-hag 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: TO MIP II. PIR; A27696, A27696. Hormone; Amidation.
                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: TO MIP I. PIR; B27696; B27696. Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6550;
                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PL 4
                          --- ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
CIP2 MYTED
ID CIP2 MYTED
AC P13737;
                                                                                                                                                                                          CIP1 MYTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscles
                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                     엄
                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                                                                                                                                                                                                                                  PSEQUENCE, AND MASS SPECTROMETRY.

RA SEGUIANCE, AND MASS SPECTROMETRY.

RA Tyler M.J., Wallace J.C.;

RT 'Intoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians.";

R. Mast. J. Chem. 49:955-963 (1996).

C. -- FUNCTION: May act as a neuromodulator or neurotransmitter.

C. -- SUBCELLULAR LOCATION: Secreted.

--- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

C. -- MASS SPECIFOMETRY: Mm.9565; METHOD=RAB.

KW Amphibian defense peptide; Amidation; Neuropeptide;

KW Pyrrolidone carboxylic acid.

PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Australian buzzing tree frog
skin peptides from Litoria
                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae, Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10; DB 1; Length 7; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9; DB 1; Length 5; Pred. No. 1.4e+05; 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
7401E9D3676046B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 - 5 AMIDATION.
5 AA; 630 MW; 668761F2C9A00000 CRC64;
                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J.,
Peptides from the skin glands of the
Litori electrica. Comparison with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rubella.",
Aust. J. Chem. 52:639-645(1999).
-!- SUBCELIULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                   Tryptophyllin 5.1.
Litoria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Litoria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA; 983 MW;
                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IP 3
                                                              TYS1 LITRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIO3 LITRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Electrin 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD RES
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
RESULT 6
TY51 LITRU
AC P82065;
DT 28-FEB-DT 28-FEB-DT 10-OCT-OCT-OC EUKARYO
OC BUKARYO
OC PELOGYION NCBI TE
RN [1] TRN [1] TRN [1] TRN SEQUENT
RA TYLER I
RT "ILCOT RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E103_LITRU
ID E103 LI
DT 28-FEB,
DT 28-FEB,
DT 10-OCT,
DE E10CT,
OC ENKATY
OC AMPAID:
OC --- SU
CC --- SU
CC --- TI
CC --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P82099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

ઠે

.. 0

Gaps

.. 0

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                          Eŭkaryota, metazoa, Mollusca, Bivalvia, Pteriomorphia, Mytiloida, Mytiloides, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.4%; Score 9; DB 1; Length 6; 50.0%; Pred. No. 1.4e+05; Live 1; Mismatches 0; Indel&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA; 621 MW; 72C9C6876DD81000 CRC64;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide II (MIP II).
Mytilus edulis (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 PL 4
```

3 PL

```
MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
(Citrobacter freundia and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine 8-amino-7-oxonomanoate aminotransferase
(BC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67:203-211(1988).
CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                  MEDLINE=97184108; PubMed=9030520;
Craig A.G., Jimenez B.C., Dykert J., Nielsen D.B., Gulyas J.,
Abogadie F.C., Porter J., Rivier J.B., Cruz L.J., Olivera B.M.
McIntosh J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID. BROMINATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 9; DB 1; Length 7; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                          Bromination; Amidation; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 7 AA; 795 MW; 6EA37DC6DB7EA6B0 CRC64;
                                                                                              28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Bromoheptapeptide Im.
                                                           7 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Prec. ...
                                                                                                                                                                                                            SYNTHESIS, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                   Conus imperialis (Imperial cone)
                                                                                     28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
1; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                      NCBI_TaxID=35631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0-0
7-0
                                                                                                                                                                                                                         TISSUE=Venom;
Md
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOA CITFR
P13071;
                                                            CONIM
                                                                                                                                                                                                            SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                           DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                      RES
                                                                     P58803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOA CITER
                                                 CONIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=P.americana;
MBDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
Starratture of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
                                                      SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Mooptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
NCBI_TaxID=6978, 6850, 6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=L.polyphemus;
MEDLINE=90287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Length 5;
                                                                                                                                                                                                                                                              InterPro; IPR005814; Aminotrans 3.
PROSITE; P800600; AA TRANSFER CIASS 3; PARTIAL.
Biotin biosynthesis; Transferage; Aminotransferase;
Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                        5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AA
                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Score 8;
Pred. No.
                                                                                                                                                                                                                               EMBL; M21922; -; NOT_ANNOTATED_CDS.
PIR; I40697; I40697.
    -!- COFACTOR: Pyridoxal phosphate.
-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=P.americana;
MEDLINE=81225865; PubMed=6113690;
O'Shea M., Adams M.E.;
                                                                                                                                                                                                                                                                                                                                                                       19.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Life Sci. 17:1253-1256(1975)
                                                                                                                                                                                                                                                                                                                                                                                                           1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                         aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOLOGICAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           : |:
1 MTT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERAM
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proctolin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRCT PERAM
ID PRCT PER
AC P01373;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                               NON TER
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
ઠ
```

. 0

Gaps

; 0

```
m
                                                                               9
                                                         5
LP --
                                    ΛÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNO6 PINPS
                                                                                                                                                                                                CIA ENTFA
P11932;
                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P81675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
UN06_PINPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                          q
                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional regulator trpl (TrpBA operon transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                    Stangier J., Dircksen H., Keller R.,
"Identification and immunocytochemical localization of proctolin in
Pericardial organs of the shore crab, Carcinus maenas.",
Peptides 7:67-72(1986).
--- FUNCTION: Stimulates cardiac output and hindgut motility,
modulates viscaral and skeletal muscle in many archropods.
--- TISSUE SPECIFICITY: Found in the lateral white neurons and in
PIR, A01644 HOROHA.
PIR: A60411.
Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JUBILIE (1:321-331)1203).

PUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPOPHAN SYNTHAGE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

SIMILARITY: Contains 1 HTH lybr-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas putida.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eberly L., Crawford 1.P.; "DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50931; HTH LYSE; PARTIAL.
Tryptophan biosynthesis; Transcription regulation; Activator;
DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 5;
1.4e+05;
                                                                                                                                                                                                                                                                                                                                                 5 AA; 649 MW; 71B7673B44600000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                 MEDLINE=86232789; PubMed=2872661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89335826; PubMed=2503057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000847; HTH_LYSR.
                                                                                                                                                                                                                                                                                                                                                                                          19.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        putida.";
Biochimie 71:521-531(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X13299; CAA31660.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       activator) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                           SPECIES=C.maenas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PPG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSEPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRPI PS
P36414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
TRPI PSEBU
ID TRPI PSEBU
ID TRPI PSEBU
OT 01-0TON-
DT 15-MARR
DE ACTIVAL
GN PREUDON
OC BECTIVAL
OC BECTIVAL
RA MEDLIN
RA EDETLIN
CC TINE
CC
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
à
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 17, Last annotation update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                          SEQUENCE.
MEDLINE=87005252; PubMed=3093276;
MOTI M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
cAM373.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 6.6, its MM is: 25 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBL_TaxID=71647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                    -!- MISCELLANBOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of needles (N141) (Fragment).
Pinus pinaster (Maritime pine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.0%; Score 8; DB 1; Length 7; 50.0%; Pred. No. 1.4e+05; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.0%; Score 8; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; cive 0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AA; 823 MW; 69D76724486B5740 CRC64;
    7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electrophoresis 20:1098-1108(1999)
                                                                                                                                                                                                                                                                                                                                            FEBS Lett. 206:69-72(1986)
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.0
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                               NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Needle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

0

Gaps

.

19.0%; Score 8; DB 1; Length 6; 50.0%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indels

Conservative

Local Similarity

Best Loca Matches

Query Match

à

2 VP :- 3 5 LP 6

g

Search completed: September 5, 2004, 11:17:30 Job time: 17 secs

human adeno human adeno human adeno gallus gall rattus norv

enterobacte

peridictyon aegilops ta bromus iner

pseudoroegn hordeum bra agropyron c

spinacia ol

henrardia p

haynaldia v taeniatheru

hordeum mar

crithopsis

P92442 1 P92226 0 P92385 P92421 P92421

psathyrosta

australopyr

thinopyrum

heteranthel

amblyopyrum hordeum vul

lophopyrum

caenorhabdí

lactobacill

bionectria

Run on:

```
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-terminus of the viral replicase (Fragment).
Cherry leaf roll virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=96124520; PubMed=8560786;
Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
"Long, nearly identical untranslated sequences at the 3' terminal
regions of the genomic RNAs of cherry leafroll virus (walnut
                                                                                                                                                                                                                                                                                                                                                                                                       Borja M.,
Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.5%; Score 17; DB 12; Length 7; 66.7%; Pred. No. 1e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800 MW; 7417672EBDC6D740 CRC64;
                                                                                                                                                                                                                                                                                                 7 AA.
                                                                                                                                                                                                                                                         ALIGNMENTS
Q9YVE3
Q9YIQ9
Q9YIR0
                        QBJJZ0
Q63668
Q47029
O34028
P83530
                                                                P83492
Q7Z1C0
P92214
P92393
P92403
P92427
P92430
                                                                                                                                098866
P92425
P92381
P92387
                                                                                                                                                                                       P92390
P92372
P92442
P92226
                                                                                                                                                                 P92210
                                                                                                                                                                         P92440
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                 P92218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virus Genes 10:245-252(1995).
 EMBL; Z34265; CAA84019.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
'... 2; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Walnut;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
NCBI_TaxID=12615;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Walnut;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLP
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TER
                                                                                                                                                                                                                                                                                                066113
                                                                                                                                                                                                                                                                                RESULT 1
066113
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBANH7 homo sapien
QBANH7 homo sapien
P9323 1ycopersico
P70804 azotobacter
P72081 nocardia la
QBG112 horrella bu
Q9553 arabidopsis
Q7624 rous sarcom
P83569 sepia offic
O50556 actinnobacil
Q54248 streptomyce
O55184 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q66113 cherry leaf
O42564 fugu rubrip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P83308 gallus gall
Q67113 influenzavi
                                                5, 2004, 11:13:09; Search time 57 Seconds (without alignments) 38.748 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                              74
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                           1017041 segs, 315518202 residues
                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q66113
O42564
P83308
Q67113
Q8NHH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBMFY6
P93233
P70804
P72081
Q8GL12
Q9C5B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q07624
P83569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             050556
054248
055184
                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                             sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mammal:*
sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                             rvirus:*
_bacteriap:*
                                                                                    US-09-761-636A-11
                                                                                                                                                                                                                                                                                                                                                                              sp archeap:*
                                                                                                                                                                                                                                                                                                                                                                                           is the number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 8 1 7 7
                                                                                                                                                                                                                                                                                                                     sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                   SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                   1 CVPLTSC 7
                                                    September
                                                                                                                                                                           seq length: 0
seq length: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74.
77.:...
19:...
                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                    Scoring table:
                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB
Maximum DB
                                                                                                   Sequence:
                                                                                                                                            Searched:
```

Database

. 0

Gaps

0;

No. Result

SCN8A.

042564

RESULT 2 042564

```
SEQUENCE FROM N.A.
MEDLINE=81001892; PubMed=7407922;
Dhar R., Chancock R.M. Lai C.-J.;
"Nonviral oligonuclectides at the 5' terminus of cytoplasmic influenza viral misny deduced from cloned complete genomic sequences.";
Cell 21:495-500(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malakooti J., Ramaswamy K.;
"Molecular cloning and characterization of the human Na+/H+ exchanger NHE-3 gene promoter region.";
Submitted (JUN-2000) to the BMBL/GenBank/DDBJ databases.
BMBL; AF282024; AAM53436.1;
SEQUENCE 7 AA; 842 MW; 74072DC772D406F0 CRC64;
                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2002 (TrEMBLrel. 22, Last annotation update)
101-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bureleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12; DB 12; Length 7; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           7 AA; 834 MW; 605EB0544EA40030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.2%; Score 11; DB 4;
100.0%; Pred. No. 1e+06;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA.
                              7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 22, TrEMBLrel. 22, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                         EMBL; M25045; AAA43202.1; -. NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                             n 28.6%;
Similarity 50.0%;
1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                           Influenza A viruses.
NCBI_TaxID=197911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                          Influenzavirus A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CV 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002
01-OCT-2002
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mini-cistron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                         (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8MFY6
Q8MFY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8NHH7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBNHH7
                                  067113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
Q8MFY6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
Q8NHH7
RESULT 4
                  067113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DI PER LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97442476; PubMed=9295353;
MEDLINE=97442476; PubMed=9295353;
Plummer N.W., McBurney M.W., Meisler M.H.;
Plummer N.W., McBurney M.W., Meisler M.H.;
M.Lernative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24008-24015 (1997).
GO; GO:0005216; F:ion channel activity; IEA.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S., "A novel active pentapeptide from chicken brain identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Bukaryota, Meopeerygii, Taleostei, Buteleostei, Neofeleostei,
Acanthomorpha, Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Takifugu.
                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NATURE 305:328-330(1983).
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.6%; Score 12; DB 13; Length 5; 66.7%; Pred. No. 1e+06; 0; Indels cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.7%; Score 15; DB 13; Length 7; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0007218; P:neuropeptide signaling pathway; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 5 AMIDATION.
5 AA; 645 MW; 69D4073767400000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AA.
     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies to FMRFamide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide; Amidation.
MOD RES 5 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, AND SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=6137771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VPL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VPL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VPL 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
```

P83308; P83308

RESULT 3 P83308

Matches

δ q

NON TER

Matches

à ద

ö

Gaps

0

0

Gaps

ö

```
STRAIN=B;
MEDLINE=96427318; PubMed=8830682;
Rehm B.H.A., Extesvag H., Valla S.;
Rehm B.H.A., Extesvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889 (1996).
EMBL; X87973; CAA61230.1;
NON TER 1
NON TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of the cmcH genes of Nocardia lactamdurans and Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephamycin biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96009872; PubMed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Liras P.;
                                                                                            Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 10; DB 2; Length 7; 33.3%; Pred. No. 1e+06; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 10; DB 2; Length 7; 66.7%; Pred. No. 1e+06; tive 1; Mismatches 0; Indels
         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
3'_methylcephem hydroxylase (Fregment).
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 162:21-27(1995).
EMBL, 221682; CAA79797.1; -.
NON TER 7 AA, 746 MW, 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23,
24,
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 33.33,
Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                             AlgT protein (Fragment)
ALGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nocardia lactamdurans.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVPLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003
01-MAR-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P72081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P72081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8GL12
Q8GL12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
P72081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8GL12
          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DA PP
                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·
0
                                               Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaes, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDILINE=97351561; PubMed=9207843;

MEDILINE=97351561; PubMed=9207843;

MEDILINE=97351561; PubMed=9207843;

Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum).";
                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol. Biol. 34:275-286(1997).
EMBL; U75692; AAC49682.1; -.
GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase .
GO; GO:0016829; F:1yase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.2%; Score 11; DB 10; Length 7; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  26.2%; Score 11; DB 8; Length 7; 50.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                                                                                                                       "Reconstruction of the evolution of trnF pseudogenes.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY015477; AAK21591.1;
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                               1 1
7 AA; 675 MW; 687451B5A76DDB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA; 828 MW; 71B412C7377415D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA
                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA.
                              Taraxacum (sect. Dioszegia) sp. 4310Hnew.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                     Taraxacum.
NCBI_TaxID=154248;
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
(Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |:
PSTN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                     PLTS 6
                                                                                                                                                                                                                                                                                            Chloroplast.
NON TER
SEQUENCE 7 #
                                                                                                                                                                                        TISSUE=Leaf;
                                                                                                                                                                                                       Mes T.H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PL
                                                                                                                                                                                                                                                                                                                                                                                                                                     3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lyase.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P93233;
```

P93233

P93233
P93233
P93233
P93233
P93233
P93233
P93233
P93233
P93233
P93233
P93233
P93233
P93233
P932333
P932333
P932333
P932333
P932333
P932333
P932333
P932333

RESULT 7

qq ð

Matches

. 0

Gaps

·,

P70804;

P70804

A D

RESULT 8

à

P70804

; 0

Gaps

0;

ö

Gaps

0

Indels

·.

6 AA.

à

```
-!- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES FURING VITELLOGENESIS. ACCUMULATES IN THE OOCYTES BEFORE BEING SECRETED DURING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OOCYTE. ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
-!- MASS SPECTROMETRY: MW=596.6; METHOD=MALDI.
                                                                                              Donze O., Spahr P.F.;
"Role of the open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBO J. 11:3747-3757 (1992).
EMBI, X67587; CAA47862.1;
SEQUENCE 7 AA, 672 MW; 776045A7687DDGFO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sperim attracting peptide SepsAP.
Sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zatylny C., Marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk spermatracting peptide.";
Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-: FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE CONTISION.
                                                                                                                                                                                                        Score 10; DB 15; Length 7;
Pred, No. 1e+06;
Rous sarcoma virus (strain Prague C).
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 6 AMIDATION.
6 AA; 597 MW; 72C8676AA0470000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyA (Fragment).
GLYA.
Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 9; DB 5;
Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                             SEQUENCE FROM N.A.
MEDLINE=93010967; PubMed=1327749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.4%;
50.0%;
                                                                                                                                                                                                                23.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                           Best_Local Similarity 50.0
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Egg;
PubMed=12207899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                             :|
6 IP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F.H.
                                                                                                                                                                                                                                                                          2 VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         050556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            050556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                      RESULT 13
P83569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                050556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                        Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                       Stevenson B., Miller J.C.;

"Comparative analyses of Borrelia burgdorferi erp genes and their cp32

"Comparative analyses of Borrelia burgdorferi erp genes and their cp32

prophages: conservation amidst diversity.";

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY142100; AAN17911.1;

GQ; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
euroèids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                          Plasmid group cp32-9.

Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Borrelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINERALITYONS; PubMed=11277426;
Wercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
"Arabidopsis thaliana genes expressed in the early compatible interacion with root-knot nematodes ";
Mol. Plant Microbe Interact. 14:288-299(2001).

EMBL; AJ286350; CAB71014.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10; DB 10; Length 7; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA; 719 MW; 6732C7287EB325D0 CRC64;
                                                                                                                                                                                                                                                                    1 1 7 AA; 849 MW; 6337244330569ED0 CRC64;
                                                                                                                                                                                                                                                                                                           Score 10; DB 2;
Pred. No. 1e+06;
1; Mismatches
                                                       Borrelia burgdorferi (Lyme disease spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JTM-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein (Fragment).
DIDI 10A-2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01,
01,
23,
                                                                                                                                                                                                                                                                                                              23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. 2)
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                         protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     е
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TSC 7
                                                                                                                                                                                                                                                                                                                                                                            1 CV 2
                                                                                                                                                                                                                                                                                                                                                                                                        1 CM 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (
01-NOV-1996 (
01-MAR-2003 (
UORF1.
                                                                                                                                                 STRAIN=N40;
                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
007624
1D 007624;
AC 007624;
DT 01-NOV-1
DT 01-NOV-1
DT 01-NAR-2
DE UORFI.
                                                                                                                                                                                                                                                       Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9C5B3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9C5B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29C5B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

; 0

Gaps

.. 0

0; Indels

7 AA.

Length 6;

```
ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 33384;
MEDLINE-9635846; PubMed=8751884;
Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
Kraig E.;
"cis Elements and trans factors are both important in strain-specific
regulation of the leukotoxin gene in Actinobacillus
actinomycetemocniteans.";
Infect. Immun. 64.3451.3460(1996).
NON TER
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=N2-3-11;

MEDLINE=2011291; PubMed=10542330;

MEDLINE=2011291; PubMed=10542330;

Medmeier U.F.;

"Analysis and regulation of the sec Y gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecA protein.";

Biochim. Biophys. Acta 1447:298-302 (1999).

Binchim. FS5915; CAA65160.1; -.

NON_TER 1

SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
 actinomycetemcomitans).
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellacee; Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces griseus.
Baceferia, Actinobacteria, Actinobacteridae; Actinomycetales;
Streptomyciaea; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                 Query Match 21.4%; Score 9; DB 2; Length 7; Best Local Similarity 33.3%; Pred. No. 1e+06; Matches 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.4%; Score 9; DB 2; Length 7; 50.0%; Pred. No. 1e+06; Ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q54248;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
RPIO protein (Fragment).
                                                                                                                                                                                                                                                                 SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                         :|:
3 LPV 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VPLT 5
                                                                                                                                                                                                                                                                                                                                                                        2 VPL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      054248
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
25424
AC 05424
AC 05424
DT 01-N0
DT 01-N0
DT 01-DE RPIO.
GN RFPIO.
OC Strep
OC Strep
OC Strep
OC STREP
CON II
RR RP SEQUE
RR REDUII
RR RP SEQUE
RR REDUII
RR REDUII
RR REDUII
RR BIOCH
DR EDUI
\overset{\circ}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Db 1 VIVT 4
```

Search completed: September 5, 2004, 11:18:34 Job time: 58 Becs

nis Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

protein search, using sw model OM protein

Run

5, 2004, 11:06:29; Search time 63 Seconds (without alignments) 31:394 Million cell updates/sec September on:

US-09-761-636A-11 Title: Perfect score:

1 CVPLTSC 7 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 segs, 282547505 residues Searched:

92273 Total number of hits satisfying chosen parameters:

length: 0 length: 7 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

29Jan04:* A Geneseq Database

geneseqp2003as:*
geneseqp2003bs:* geneseqp1990s:* geneseqp2001s:* geneseqp2002s:* geneseqp2000s:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

	Description	Contraction of the Contraction o	Vidao:		bhage r	Aaul0724 Kidney bo	7 Kidney	0 Kidney	9 Kidney	VEGE No	1000	α	ים מכ	٠.			* <	 	o Cadher	S IGF-1	Aay85404 IL-2 deri	Aay61930 Cadherin-	œ	~		ο σ	۰ ۵
SUMMARIES	ID	AAU04530	AAW13421	AAB12007	AAE11813	AAU10724	ABU59533	ADC33700	ADC33699	AAU04531	ABJ00550	ABG33862	AAY61489	AAY62764	AAY62007	AAY62224	AAY85374	ABV64260	AAP51449	ANVORACA	#0#001W	AAY61930	AAY62758	AAY64322	AAY61506	AAY62489	AAY63236
	DB 1	4	N -	<u>س</u>	4	2	9	7	7		Ŋ	Ŋ		m	m	m	-									ო	m
-40	Query Match Length	100.0	73.8	73.8	73.8	73.8	73.8	73.8	73.8	9 0.69		. 7	6.	59.5	59.5	59.5	57.1		54.8	α) c	0.0	20.	æ.	54.8	4.8	54.8 7
	Score	42	31	31	31	31	31	31	31	29	28	28	56	25	25	25	24	24	23	23		7 (23	23	23	23	23
	Result No.	1	7	e	4	2	9	7	00	6	10	11	12	13	14	15	16	17	18	19	00	9 6	17	7.7	23	24	25

Abb47076 Desmocoll Aar15772 Farnesyl- Aar49769 Farnesylt Aaw77833 Parnesylt Aaw64459 Farnesyl Aaw67428 HCV Deptin Ab137236 Rhodopsin Aar36871 Insulin-1 Aar43615 Peptide d Aaw67430 HCV Deptin Aay64307 Cadherin- Aay64307 Cadherin- Aay64235 Cadherin- Aay62135 Cadherin- Aay62135 Cadherin- Aay63266 Protocadh Abb46174 Desmoglei Ab104536 Molt-4 le	
5 ABB47076 2 AAR15772 2 AAR49769 2 AAR49769 2 AAR67428 2 AAW67428 6 ABJ37236 2 AAR36871 2 AAR43615 2 AAR674307 3 AAY64292 3 AAY64292 3 AAY62135 3 AAY62135 5 ABB46114	2 AAW60386 2 AAW93712 3 AAB03612 3 AAX64262
	20.00
555555555555555555555555555555555555555	2222
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 2 6 4 8

ALIGNMENTS

AAU04530 standard; peptide; 7 AA. VEGF based monocyclic peptide 8. (first entry) 26-SEP-2001 AAU04530; AAU04530

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic

Location/Qualifiers
1. .7
/note= "This bond cyclises the peptide" Key Disulfide-bond

WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES. Achen MG,

Stacker S, Hughes RA, WPI; 2001-442248/47

Cendron A;

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

```
peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, conversion or lymphangiogenesis in a mammal with a condition contaction or lymphangiogenesis in a mammal with a condition contaction is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive correction. The peptides are also used to modulate vascular permeability in faction induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoned cavity, pleura, cor brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF corp and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obtaining compound that homes to selected organ or tissue - by in vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide (s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homing peptide; in vivo panning; screening; phage display;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 42; DB 4; L
100.0%; Pred. No. 1.4e+06;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 16; Page 68; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW13421 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00526708.
95US-00526710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US014600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kidney homing peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-202359/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidney homing
drug delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruoslahti E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9710507-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW13421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

This synthetic peptide is a claimed example of a kidney-homing peptide that was identified using a novel method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically

```
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying and recovering organ homing molecules or peptides by in vivo panning comprises administering a library of diverse peptides linked to a tag which facilitates recovery of these peptides.
                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a mouse kidney homing peptide. This sequence was identified by using in vivo panning to screen a library of potential organ homing molecules. The present sequence can be used to direct a moiety to a kidney tissue, by linking the moiety to the present sequence. Examples of potential moieties are drugs, toxins or a detectable label
involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue. S. .g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAWI341-52, AAWI1181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they maintain specificity in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kidney, homing peptide; organ targeting; tissue targeting; mouse; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                     .;
0

    .7
/note= "Can optionally form a cyclic peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.8%; Score 31; DB 3; Length 7; 57.1%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                     Length 7;
                                                                                                                                                                                     Score 31; DB 2; I
Pred. No. 1.4e+06;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Col 18; 20pp; English
                                                                                                                                                                                                                                                                                                                                                          AAB12007 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00526710.
97US-00813273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-00862855.
                                                                                                                                                                                          73.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruoslahti E;
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kidney homing peptide # 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-410850/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVPLTSC 7
                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                      1 CVPLTSC
                                                                                                                                                                                                                                                                                 CLPVASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasqualini R,
                                                                                                                                                              Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6068829-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                             AAB12007;
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                               RESULT 3
                                                                                                                                                                                                                                                                                                                                                 AAB12007
                                                                                                                                                                                                                                                                                                                                                                                           δ
            8888888888%
                                                                                                                                                                                                                                                                                    du
                                                                                                                                                                                                                                                           ò
```

Organ targeting; tissue targeting; cancer; tumour homing molecule; delivery of target molecule; kidney homing peptide. Kidney homing peptide #1 useful for delivery of target molecules.

95US-00526710. 97US-00813273. 97US-00862855.

Pasqualini R;

Ruoslahti E,

WPI; 2002-040196/05.

(BURN-) BURNHAM INST

23-JUN-1997;

99US-00227906

08-JAN-1999;

23-OCT-2001

US6306365-B1

Synthetic.

```
The invention relates to an enriched library fraction containing molecules that selectively home to a selected organ or tissue such as brain, kidney or tumour recovered by in vivo panning. The invention generally relates to the field of molecular medicine, drug delivery and to a method of invivo panning for identifying a molecule that homes to a specific organ. The molecules, e.g., peptides, peptidomimetics, proteins and fragments of proteins contained in an enriched library fraction may treat disease or in diagnostic methods. The present sequence is a peptide from bacteriophage targetted to kidney. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                     Enriched library fraction; brain; kidney; tumour; panning; diagnostic; molecular medicine; drug delivery; peptidomimetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enriched library fraction comprising molecules recovered by in vivo panning that selectively home to a selected organ or tissue useful for treating disease or in diagnostic methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.8%; Score 31; DB 4; Length 7; 57.1%; Pred. No. 1.4e+06; ive 2; Mismatches 1; Indels
                                                                                                                                                                            Phage peptide #21 targetted to kidney.
                                                                              AAE11813 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Col 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           97US-00813273.
97US-00862855.
                                                                                                                                                                                                                                                                                                                                                 99US-00226985,
                                                                                                                                                                                                                                                                                                                                                                         95US-00526710
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ж
Ж
                                                                                                                                                                                                                                               unidentified bacteriophage.
Unidentified.
                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pasqualini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                               (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-610691/70.
|:|: ||
CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|: ||
CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVPLTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruoslahti E,
                                                                                                                                                                                                                                                                                        US6296832-B1
                                                                                                                                                                                                                                                                                                                                              08-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1997;
                                                                                                                                    11-SEP-2003
                                                                                                                                                  18-DEC-2001
                                                                                                                                                                                                                                                                                                                     02-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                          AAE11813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
```

```
The present invention relates to a method of recovering molecules that home to a selected organ or tissue. The method comprises administering to the subject the library of diverse molecules, collecting a sample of the selected organ or tissue (e.g. brain or kidney), and recovering from the sample several molecules that home to the selected organ or tissue. The method is useful for identifying molecules, particularly useful for method is useful for a target molecule is useful for e.g. raising an appearance of molecule is useful for e.g. raising an entibod specific for a target molecule, targeting a desired moiety (e.g. drug, toxin or detectable label) to the selected organ. Specifically, the method is useful for identifying the presence of cancer in a subject by linking an appropriate moiety to a tummour homing molecule. The present specifically home to a selected organ and, therefore provides a method provides a direct means for identifying molecules that a method and advantage over previous methods, which require that a molecule identified using an in vitro screening method subsequently be avained to determine if it maintains its specificity in vivo. AAU10724-invanrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                         Recovering molecules that home to an organ or tissue, useful for identifying molecules that home to a specific organ or tissue, e.g. identifying a tumor homing molecule to identify the presence of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%; Score 31; DB 5; Length 7; 57.1%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kidney receptor targeting peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Col 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU59533 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                            by in vivo panning of a library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|: ||
CLPVASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU59533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU59533
g
```

·;

Gaps

0;

AAU10724 standard; peptide; 7 AA.

12-MAR-2002

AAU10724;

AAU10724 ID AAU1 XX AC AAU1 XX DT 12-N

RESULT 5

Synthetic

Unger EC,

```
described: (1) a nucleic acid molecule comprising a sequence encoding the recombinant chimeric envelope protein; (2) a vector comprising a nucleic acid sequence encoding the chimeric envelope protein; (3) a recombinant conversion a acid sequence encoding the chimeric envelope protein (3) a recombinant conversion and con
                                                                                                                                                                                                                                                                                                                                                                  New chimeric retrovirus envelope protein comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a chimeric retrovirus envelope protein (I) comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeric retrovirus envelope protein; ecotropic envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%; Score 31; DB 7; Length 7; 57.1%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kidney cell targeted peptide SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 4; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADC33699 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene therapy; cancer
                                                                             07-MAR-2003; 2003WO-US007323
                                                                                                                                       08-MAR-2002; 2002US-0362655P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                     (UYMA-) UNIV MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                            Gollan TJ;
                                                                                                                                                                                                                                                                                                                    WPI; 2003-722332/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003076596-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-2003.
                           18-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                            Green MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC33699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC33699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a composition comprising a bioactive agent chomogeneously dispersed in a targeted matrix (polymer and targeting chomogeneously dispersed in a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, choice composition and treating cancer comprising administration of the composition. The method is useful for targeted delivery of a drug, cope composition. The method is useful for targeted delivery of a drug, capecially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides are disclosed including cathepsin-D Examples of targeting fibronectin- and vitronectin-binding integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies, peptides targeting the analogenic endothelium of foolid tumours, tissue specific peptides (e.g. of lung, skin, panoreas, intestine, uterus, advenal gland and retina), and cationic cancer-targeting peptides. The present sequence is a peptide targeting ligand disclosed in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy.
   cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor; fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium; tumour; cationic cancer-targeting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric retrovirus envelope protein; ecotropic envelope protein; cytostatic; gene therapy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.8%; Score 31; DB 6; Length 7; 57.1%; Pred. No. 1.4e+06; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ramaswami V, Romanowski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidney cell targeted peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC33700 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; Page 38; 46pp; English.
                                                                                                                                                                                                                                                                                                    25-JUL-2001; 2001US-00912609.
                                                                                                                                                                                                                                                                                                                                                               05-JAN-2000; 2000US-00478124
                                                                                                                                                                                                                                                                                                                                                                                              31-OCT-2000; 2000US-00703474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsunaga TO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNGE/) UNGER E C.
(MATS/) MATSUNAGA T O.
(RAMA/) RAMASWAMI V.
(ROMA/) ROMANOWSKI M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-208921/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLPVASC 7
                                                                                                                                                                                        US2002041898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7 AA;
                                                                                                                                                                                                                                                11-APR-2002.
```

.; 0

Gaps

; 0

i; Indels

08-MAR-2002; 2002US-0362655P. 07-MAR-2003; 2003WO-US007323

WO2003076596-A2

Synthetic.

ADC33700;

RESULT 7

à a Cendron A;

Stacker S,

```
Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

    .6
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            AAU04531 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                     VEGF based monocyclic peptide 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                           1 CVPLTSC 7
                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                        1 CLPVASC 7
                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
              Green MR,
                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                         AAU04531;
                                                                                                                                                                                                                                                             Watches
                                                                                                                                                                                                                                                                                                                   AAU04531
ID AAU0
δ
```

diabetic retinopathy

```
The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vegep (vascular endothellal growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betactor of the carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with a least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, concattrised by angiogenesis, newscularisation or lymphangiogenesis; newscularisation or lymphangiogenesis in a mammal with a condition is diabetic retinopathy, psoriasis, arthropathy, confined monocyclic cerebrovascular accident, post-angioplasty restenosis, head, heat or cold craume substance induced newscularisation of the liver, excessive conformance induced newscularisation of the liver, excessive conformance induced newscularisation of the liver, excessive
                                                                                                                                                                                                                Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has or on lungs, peritoneal spring or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or D and extrait inflammation, especially rheumatoid arthritis, psoriasis and although and and inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                              Claim 49; Page 32; 102pp; English.
                    (LUDW-) LUDWIG INST CANCER RES
                                                                                       Achen MG, Hughes RA,
                                                                                                                                                    WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                  residues
                       The present invention describes a chimeric retrovirus envelope protein of (1) comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein. Also described: (1) a nucleic acid molecule comprising a sequence encoding the recombinant chimeric envelope protein; (2) a vector comprising a nucleic acid sequence encoding the chimeric envelope protein; (3) a recombinant retroviral particle comprising a chimeric envelope protein; (3) a recombinant chimeric envelope protein; (3) a recombinant retroviral particle acid sequence encoding the chimeric envelope protein comprising a identifying a nucleic acid sequence encoding the chimeric envelope protein comprising a continuity and call ind (6) treating cancer. (1) has cytostatic acid sequence to a cell; and (6) treating cancer. (1) has cytostatic acitivity and can be used in gene therapy. The chimeric retrovirus envelope protein is contrained and infecting the cancer cell with a virus, e.g. cretrovirus comprising the chimeric envelope protein comprising a heterologous short peptide ligand and a therapeutically useful gene, e.g. encoding thymidine kinase. The present sequence represents a kidney cell contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                         New chimeric retrovirus envelope protein comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 7; Length 7;
Pred. No. 1.4e+06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 3; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.8%;
57.1%;
(UYMA-) UNIV MASSACHUSETTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                               Gollan TJ;
                                                                                                                               WPI; 2003-722332/68.
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemia; graft-versus-höst disease; neurodegenerative disease; immunosuppressive; nephrotropic; antirheumatic; antiarthritic; neuroprotective, cytostatic; immunostimulant; antitumour; anti-HIV; antiasthmatic; antiallergic; immunostimulant; antianemic; haemostatic; dermatological; antiinflammatory; cardiant; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.
                                                                                                                                                                                                                                                                                                                                                                 B lymphocyte stimulator protein binding protein; BLyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting;
                                                                        Gaps
                                                                        0
                                                                     0; Indels
                                  69.0%; Score 29; DB 4; Length 6; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             B lymphocyte stimulator protein binding peptide #1.
                                                                                                                                                                                                                          ABJ00550 standard; peptide; 7 AA.
          Query Match
Best Local Similarity 100...
Best S; Conservative
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                      1 CVPLT 5
Sequence 6 AA;
                                                                                                                                        1 CVPLT
                                                                                                                                                                                                                                                                                              05-SEP-2002
                                                                                                                                                                                                                                                             ABJ00550;
                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                          ABJ00550
                                                                                                      à
                                                                                                                                   g
```

Unidentified

```
18-AUG-2000; 2000US-0226489P.
                               (DYAX-) DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-1998;
06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-NOV-11999
                                                            Beltzer JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY61489;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the treatment, prevention or ameliozation of a disease or disorder associated with: aberrant B lymphocyte stimulator (BLyS), BLyS receptor expression or activity; cells of hematopoietic origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation and graft rejection involving administration of BLyS binding polypeptide. The BLyS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases of cells of hematopoietic origin, graft rejection, allergies, infectious diseases, arteriosclerosis, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a Blymphocyte stimulator protein binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B Lymphocyte Stimulator protein; B Lymphocyte Stimulator binding peptide; BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid; synovial fluid; saliva; mucus.
                                                                                                                                                                                                                                                                                                             The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B Lymphocyte stimulator binding polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 5; Length 7; Pred. No. 1.4e+06; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B Lymphocyte Stimulator (BLyS) binding peptide #436.
                                                                                                                                                                                                                                                        Rosen CA;
                                                  label= Phe, Trp, Tyr
                                                                                                                                                                                                                                                        Fleming TL,
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          Claim 69; Page 233; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG33862 standard; peptide; 7 AA.
                                                                                /label= Pro, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-AUG-2001; 2001WO-US025891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.78;
57.18;
                                                                                                                                                                    17-AUG-2001; 2001WO-US025850.
                                                                                                                                                                                               18-AUG-2000; 2000US-0226700P
                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                         Potter DM,
                                                                                                                                                                                                                                                                                    WPI; 2002-499775/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC 7
                                      Misc-difference
                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200216412-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
                                                                                                             WO200216411-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2002.
                                                                                                                                                                                                                                                           Beltzer JP,
                                                                                                                                          28-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG33862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG33862
```

à 셤

```
Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; protocadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
                                                                                                                                      New B-lymphocyte stimulator binding polypeptide useful in detecting or isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
                                                                                                                                                                                                                                                                                                                                             The invention relates to a B Lymphocyte Stimulator (BLyS) binding polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins reversibly or irreversibly. The binding peptides are used in detection, isolation and/or purification of BLyS in a solution such as water or a buffer solution, as well as any fluid and/or cell obtained from an individual blodgical fluid, body tissue, body cell, cell line, tissue culture or other source containing BLyS or BLyS-like polypeptides. The blodogical fluids include sera, plasma, lymph, blood, blood fraction, urine, synovial fluid, spinal fluid, saliva and mucous. Sequences ABG33465-33415, ABG33423-33575, ABG33588-33846, ABG33848-33850 and ABG33852 represent BLyS binding peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%; Score 28; DB 5; Length 7; 57.1%; Pred. No. 1.4e+06; ive 0; Mismatches 3; Indels
Ladner RC,
                                                                                                                                                                                                                                                                                           Disclosure; Page 132; 269pp; English.
   Fleming TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 1. .7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY61489 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-CA000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disease; cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
       Potter MD,
                                                                            WPI; 2002-351647/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CXPXTGC 7
```

.. O

```
New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diod vessel regression in a creating drug delivery to the central nervous system, treating a demyelinating drug delivery to the increasing vasoperameability in a mammal, enhancing adhesion of anonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for reacting e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAY6052 to AAY64572 represent specifically claimed peptides, and AAX64573 to AAX64573 and AAX33183 to AAX33186 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                               The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in amammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting anglogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obseity in a mammal, stimulating
                                                                                                                                                                                                                                                                  Claim 36; Page 172; 252pp; English.
(ADHE-) ADHEREX TECHNOLOGIES INC
                                                             Byers S;
                                                          Gour BJ,
                                                                                                         WPI; 2000-038791/03
                                                       Blaschuk OW,
```

Sequence 7 AA;

Gaps .; 0 3; Indels Length 7; 61.9%; Score 26; DB 3; I 57.1%; Pred. No. 1.4e+06; 0; Mismatches 4; Conservative Query Match Best Local Similarity 1 CVPLTSC 7 Matches à

0

1 ČEPKTGĆ 7 g

AAY62764 standard; peptide; 7 AA. AAY62764; RESULT 13 AAY62764

(first entry) 02-MAR-2000

PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.

Modulation; nonclassical cadherin mediated cell adhesion; CAR; hibbition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-12; cadherin-15; T-cadherin; PB-cadherin; cadherin-15; T-cadherin; D-cadherin; desmoglein; desmocollin; called neuronal receptor; LI-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.

Synthetic.

Homo sapiens

Location/Qualifiers Disulfide-bond

WO9957149-A2

```
The present invention describes caunting modulating agence (mapprising peptides which comprise a nonclassical cadherin cell adhesion recognition (GAR) sequence. The MAS can be used for modulating cadherin-mediated functions They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug through the skin of a mammal, compared to a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, stimulating angiogenesis in a mammal, enhancing drug delivery to the expressing cell, preventing or treating obesity in a mammal, stimulating contral nervous system, treating a demyelinating adversor to the increasing vasopermeability in a mammal, enhancing drug delivery to the increasing vasopermeability in a mammal, enhancing advestion of contral nervous system, treating a demyelinating synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for can conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for detection and diabetes The conducts can also be used for detection and diagnosis and in bioreactors. AAV66132 to AAV64512 represent specifically claimed peptides, and the answer of the answer.
                                                                                                                                                                                                                                                                                                                                                     New cadherin modulating agents, used for modulating nonclassical cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; protocadherin; cadherin; desmecognition; cadherin; calcing binding; cancer; tumour; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                            -mediated functions for treating e.g. cancers, obedity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes cadherin modulating agents (MA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 3; Length 7; Pred. No. 1.4e+06; 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 72; Page 193; 252pp; English.
                                                                                                                                                                                                                       (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY62007 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                          98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
                                                                   99WO-CA000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                   Gour BJ,
                                                                                                                                                                                                                                                                                                             WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDPKTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                                                                                                                                                                                                                               Blaschuk OW,
                                                              05-MAY-1999;
                                                                                                                                                                         08-MAR-1999;
                                                                                                                                                      20-JAN-1999;
                                                                                                             05-MAY-1998
                                                                                                                                 06-NOV-1998
                         11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY62007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY62007
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ö

02-MAR-2000 (first entry)

Location/Qualifiers

```
New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                         present invention describes cadherin modulating agents (MA)
rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                            Claim 48; Page 180; 252pp; English
                                                                                                                                                   (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                  Blaschuk OW, Gour BJ,
                                                                                                                                                                                WPI; 2000-038791/03
                                                     Digulfide-bond
                                                                      WO9957149-A2
                                Homo sapiens
                                                                                                  05-MAY-1999;
                                                                                                                        06-NOV-1998;
                                                                                                                 05-MAY-1998;
                                                                                                                                     08-MAR-1999
                                                                                    11-NOV-11999
                          Synthetic
```

Byers S;

98US-00073040. 98US-00187859. 99US-00234395. 99US-00264516.

99WO-CA000363

```
comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating recognition (CAR) sequence. The MAs can be used for modulating cancerosing callesial acaderin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, chancing delivery of a drug through the skin of a mammal, can mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting of anylogenesis in a mammal, inhibiting observed in a mammal, stimulating cancer in a mammal, inhibiting anylogenesis in a mammal, inhibiting apoptosis in a nonclassical cadherin-expression in a mammal, enhancing drug delivery to the contral nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing symaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating enclise, inhibiting symaptic stability in conclassical cadherin-expressing cells, inhibiting symaptic stability in a mammal. They can also be used for treating enclised for in a conclassical dependence or enhancing adhesion of foreign tissue in a conformal degeneration, multiple sclerosis and diabetes. The products can also be used for treating enclassis, arthritis, and packed the conclassis and in bioreactors. Anylossy to the conclassion of the conclassion in the conclassion of the conclassion in the conclassion of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.5%;
```

```
Score 25; DB 3; Length '; Pred. No. 1.46+06;
                                                   4; Conservative
                           Query Match
Best Local Similarity
Matches 4; Conserv
Sequence 7 AA;
```

```
AAY62224 standard; peptide; 7 AA.
CDPKTGC
                           RESULT 15
AAY62224
ID AAY62:
XX
AC AAY62
g
```

AAY62224;

1 CVPLTSC 7

⋧

```
The present invention describes cadherin modulating agents (WA)

Comprising peptides which comprise a nonclassical cadherin cell adhesion

recognition (CAR) sequence. The MAs can be used for modulating of

conclassical cadherin-mediated functions. They can be used for e.g.

conclassical cadherin-mediated functions. They can be used for e.g.

conclassical cadherin-mediated functions. They can be used for e.g.

conclassing delivery of a drug through the skin of a mammal, training conclassing delivery of a drug through the skin of a mammal, inhibiting metastasis of a cancer in a mammal, trainibiting cappenesis in a mammal, trainibiting conclassing call, preventing or treating obesity in a mammal, stimulating concrassing vasopermeability in a mammal, enhancing drug delivery to the conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age correlated macular degeneration, multiple sclerosis and diabetes. The mammal. They can also be used for treating e.g. psoriasis, arthritis, age conclucts can also be used for treating e.g. psoriasis, arthritis, and mammal. They can also be used for treating e.g. psoriasis, arthritis, age conclucts can also be used for treating e.g. psoriasis, arthritis, and mammal. They can also be used for detection and diabetes. The conclucts can also and AAX53186 represent sequences used in the conclusion of conclusions and in bioreacces. AAX66572 represent specifically claimed peptides, and in bioreacces in the conclusion of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                         Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-15; T-cadherin; PB-cadherin; cadherin, related neuronal receptor; II-cadherin; protocadherin; desmocallin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 54; Page 184; 252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00073040.
98US-00187859.
99US-00234395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-CA000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-038791/03
                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-11999
                                                                                                                                                                                                                                                                                                                    Synthetic
```

4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

Sequence 7 AA;

ö

Gaps

.

59.5%; Score 25; DB 3; Length 7; 57.1%; Pred. No. 1.4e+06; ive 0; Mismatches 3; Indels

ð

qq

Search completed: September 5, 2004, 11:17:09 Job time : 64 secs

This Page Blank (uspto)

```
Sequence 7, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 8, Appli
Sequence 1375, Ap
Sequence 1375, Ap
Sequence 1375, Ap
Sequence 3971, Ap
Sequence 4047, Ap
Sequence 4047, Ap
Sequence 4047, Ap
Sequence 2371, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Appl
Sequence 7, Appli
                                                                                                               5, 2004, 11:18:40; Search time 66 Seconds (without alignments)
33.416 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "cgn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB.pep:*
"cgn2_6/ptodata/2/pubpaa/DS05 PUBGOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US06_PUBGOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
"cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
"cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
"cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
"cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
"cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-912-609-7-1
US-09-912-609-7-2
US-09-912-613-8
US-09-912-813-8
US-10-006-869-1375
US-10-006-869-1375
US-10-006-869-1799
US-10-006-869-1799
US-10-006-869-1799
US-10-106-869-1799
US-10-106-869-1799
US-10-106-869-1799
US-10-106-869-1799
US-10-106-869-1799
US-10-106-869-1799
US-10-1795-0132-1799
US-10-1795-0132-1799
US-10-1795-0132-1799
US-10-1795-0132-1799
                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-761-636A-11
                                                                                                                                                                                                                                                                                                                               1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Applications AA:*
                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                            Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                           US-09-761-636A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length I
                                                                                                                                                                                                                               1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published
                                                                                                                    September
                                                                                                                                                                                                                                                                      BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.0
66.7
66.7
661.9
61.9
59.5
59.5
                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
```

equence 3574, equence 1392, equence 1740, equence 2155,	Sequence 3637, Ap Sequence 1641, Ap Sequence 11922, Ap Sequence 1192, Ap Sequence 2155, Ap Sequence 2155, Ap Sequence 221, App Sequence 221, App Sequence 225, App Sequence 225, App Sequence 21888, Ap Sequence 2750, Ap Sequence 2750, Ap Sequence 2750, Ap Sequence 2750, Ap Sequence 1888, Ap Sequence 184, App Sequence 188, App Sequence 183, App Sequence 188, App Sequence 1	
US-10-395-032-3 US-10-006-869-1 US-10-006-869-1 US-10-006-869-2	US-10-006-869-363 US-10-006-869-363 US-10-395-032-2154 US-10-395-032-2155 US-10-395-032-2155 US-10-395-032-2155 US-10-395-032-265 US-10-083-84-35 US-09-792-286-221 US-09-792-286-225 US-09-792-286-225 US-09-792-286-225 US-10-006-869-3606 US-10-006-869-3606 US-10-006-869-3606 US-10-395-032-3606 US-10-395-032-3606 US-10-395-032-3606 US-09-911-838-184 US-09-911-838-184 US-09-765-086-103	
2444	11111111111111111111111111111111111111	
~~~~	rrrrrrrrrrrr	
3 54.	233 54.8 223 33 54.8 222 223 35.4.8 222 222 222 524.8 222 222 522 52.4.4.8 222 522 522 522 52.4.4.4.8 222 522 522 522 522 522 522 522 522 522	
16 17 18 19	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

# ALIGNMENTS

```
US-09-761-636A-11

Sequence 11, Application US/09761636A

Patent No. US2002065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: ACHEN, Marc

APPLICANT: GENERAL, SICHARD

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR PAPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR PILING DATE: 2000-05-16

SEQ ID NOS: 34

SEQ ID NO 11

TYPE: PRT

ORGANISM: Home sapiens

US-09-761-636A-11

QUery Match

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

OY 1 CVPLTSC 7

Db 1 CVPLTSC 7
```

.. 0

> RESULT 2 US-09-912-609-7 ; Sequence 7, Application US/09912609 ; Publication No. US20020041898A1

ö

Gaps

```
y Sequence 8, Application US/09932613

y Sequence 8, Application No. US20030091565A1

publication No. US20030091565A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Petter, James P. .

APPLICANT: Petter, Tony J.

APPLICANT: Petter, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: Dyx-025.1 PCT; DXX-025.1 US

FULL REFERENCE: Dyx-025.1 PCT; DXX-025.1 US

CURRENT APPLICATION NUMBER: US/99/932,613

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SEQ ID NO 8

LENGTH: 7

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09761636A

Sequence 12, Application US/09761636A

Patent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Marc

APPLICANT: ACHEN, Marc

APPLICANT: CENDRON Angela

TILLE OF INVENTION Angela

TILLE OF INVENTION VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE REFERENCE: 1064/48505 Achen et al

CURRENT APPLICATION NUMBER: US/09/761,636A

CURRENT FILING DATE: 2000-01-18

PRIOR PILING DATE: 2000-01-16

PRIOR FILING DATE: 2000-01-16

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
0
                                                                                                                                                                                                                                                                                                            ·;
                                                                                                                                                                                                                                                      Score 31; DB 12; Length 7; Pred. No. 1.2e+06; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%; Score 29; DB 9; Lk
100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0;
                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
TELEPHONE: (619) 535-9001
                      TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                 Query Match 73.8%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
, ORGANISM: Homo sapiens
US-09-761-636A-12
                                                                                                                                                                                                                                                                                                                                                                                                     |:|: ||
1 CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                    1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVPLT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-09-761-636A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-09-932-613-8
                                                                                                                                                                                                                     US-09-922-227-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                         à
                                 APPLICANT: UNGER, EVAN C.
APPLICANT: WATSUNGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
APPLICANT: RAMASWAMI, VARADARAJAN
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFREENCE: 5030-0001_20
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT FILING DATE: 2001-07-25
FRIOR APPLICATION NUMBER: 09/703,474
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PALCELIN VEY. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/0992227
Sequence 21, Application US/0992227
Publication No. US20040071689A1
GENERAL INFORMATION:
APPLICANT: Renation Fargualini, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
Home to a Selected Organ In Vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.8%; Score 31; DB 12; Length 7; 57.1%; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TIM PC compatible
COMPUTER: TIM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/922,227
FILING DATE: 02-Aug-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,710
FILING DATE: 11-5EP-1995
APPLICATION NUMBER: US 08/813,273
FILING DATE: 10-MAR-1997
APPLICATION NUMBER: US 08/862,855
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: US 09/227,906
FILING DATE: 08-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,915
REFERENCE/DOCKET NUMBER: P-LJ 4859
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|: ||
1 CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-922-227-21
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
```

à 셤 . 0

Gaps

ö

```
Sequence 1375, Application US/10395032
| Publication No. US20030229199A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. APPLICANT: Symonds, James Matthew
| APPLICANT: Symonds, James Matthew
| APPLICANT: Symonds, James Matthew
| APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
| TITLE OF INVENTION: CADHERIN MEDIATED FUNCTIONS
| FILE REFRENCE: 100086, 407C9
| CURRENT APPLICATION NUMBER: US/10/395,032
| CURRENT FILING DATE: 2003-03-21
| NUMBER OF SEQ ID NOS: 4052
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 1375
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BLANCHAK, Orest W. APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew TAPLICANT: GOUY, BATABATA J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS FILE REPERENCE: 100066.40707 CURRENT APPLICATION NUMBER: US,10/006,869 CURRENT FILING DATE: 2001-12-03 SOFTWARE: PATENTIN VOET: 2.0 SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                             OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-7 cell adhesion recognition sequence US-10-395-032-1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Representative cyclic modulating agent based on
                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.9%; Score 26; DB 15; Length 7; Best Local Similarity 57.1%; Pred. No. 1.2e+06; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                  Score 26; DB 14;
Pred. No. 1.2e+06;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1799, Application US/10006869
Publication No. US20030082166A1
GENERAL INFORMATION:
                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                h 61.9%;
Similarity 57.1%;
4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
               SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                 1 CEPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CEPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC
                                                                                                                                                                                                               US-10-006-869-1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-395-032-1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-006-869-1799
                                      SEQ ID NO 1375
LENGTH: 7
                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dyax Corp.
APPLICANT: Dyax Corp.
APPLICANT: Dotter, James P.
APPLICANT: Detter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REPERENCE: Dyav-018.1 PCT; DXX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-10-006-869-1375

US-10-006-869-1375

Sequence 1375, Application US/10006869

Publication No. US20030082166A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

ITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

ITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086-407C7

CURRENT APPLICATION NUMBER: US/10/006,869

CURRENT FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                            Trp, or Tyr (preferably Tyr);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAWE/KEY: MISSIANDE DIVIDED FOLYPEDINGE
1.0CATION: (2)...(2)
COTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
NAME/KEY: MISSC FEATURE
1.0CATION: (4)...(4)
COTHER INFORMATION: X4 is Pro or Tyr (preferably Pro);
US-09-932-322-8
                                                                                                                                                                                                                                                                          66.7%; Score 28; DB 10; Length 7; 57.1%; Pred. No. 1.2e+06; 1.1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 28; DB 10; Length 7; 57.1%; Pred. No. 1.2e+06; ative 0; Mismatches 3; Indels
                                         OTHER INFORMATION: BLyS binding polypeptide
NAME/KRY: MISC_FEATURE
OCACION: (2): (2)
OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably NAME/KRY: MISC_FEATURE
ICCATION: (4): (4)
COLATION: (4): (4)
US-09-932-613-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: BLyS binding polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.1%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                             1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                           1 CXPXTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CXPXTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-09-932-322-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                             ģ
                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

q à

ò.

```
| Sequence 3971, Application US/10395032 |
| Sequence 3971, Application US/10395032 |
| Publication No. US2003022919941 |
| GENERAL INFORMATION: Great W. |
| APPLICANT: Blaschuk, Orest W. |
| APPLICANT: Blaschuk, Orest W. |
| APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL |
| TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS |
| TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS |
| TITLE OF INVENTION OF A0709 |
| CURRENT TILING DATE: 100086.40709 |
| CURRENT TILING DATE: 2003-03-21 |
| NUMBER OF SEQ ID NOS: 4052 |
| SOFTWARE: PATENTIN VEY: 2.0 |
| SEQ ID NO 3971 |
| TENNOW: 7
                                                                                                                                                          US-10-395-032-1799

i Sequence 1799, Application US/10395032

j Sequence 1799, Application US/10395032

j Sequence 1799, Application US/10395032

j Bublication No. US20030229199A1

j GENERAL INFORMATION:

j APPLICANT: Symonds, James Matthew

j APPLICANT: Symonds, James Matthew

j TILLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

j TILLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

j TILLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

j TILLE OF INVENTION NUMBER: US/10/395,032

j CURRENT APPLICATION NUMBER: US/10/395,032

j SOFTWARE: PATENTIN VET: 2:03-03-03-21

j SOFTWARE: PATENTIN VET: 2:0

j SOFTWARE: PATENTIN VET: 2:0

j SOFTWARE: PATENTIN VET: 2:0

j SOFTWARE: PATENTIN VET: 2:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-10-395-032-3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Representative cyclic modulating agent based on corner INFORMATION: cadherin-12 cell adhesion recognition sequence US-10-395-032-1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.5%; Score 25; DB 15; Length 7; 57.1%; Pred. No. 1.2e+06; iive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.5%; Score 25; DB 15; Length 7; Best Local Similarity 57.1%; Pred. No. 1.2e+06; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CDPKTGC 7
CVPLTSC 7
                                                         1 CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-395-032-4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-395-032-3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
         ò
                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-006-869-4047
; Sequence 4047, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Broands, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PATENTIN VEY. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3971, Application US/10006869

Publication No. US20030082166A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
ANDERNIE APPLICATION NOWBER: VS/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE PARENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:

; OTHER INFORMATION: Representative cyclic modulating agent based on

; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence

US-10-006-869-4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
      ; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-10-006-869-1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                              Score 25; DB 14; Length 7;
Pred. No. 1.2e+06;
                                                                                                                                                       3; Indels
                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                 Query Match 59.5%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CDPKTGC 7
                                                                                                                                                                                                                       1 CVPLTSC 7
                                                                                                                                                                                                                                                                          1 CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-006-869-3971
                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-006-869-3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEO ID NO 4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                 a
```

°;

Gaps

., 0

Ö

Gaps

·.

```
;
0
; Sequence 4047, Application US/10395032; Publication No. US2003022919941; Publication No. US2003022919941; GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew, APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C9; CURRENT APPLICATION NUMBER: US/10/395,032; CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
: LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3574, Application US/10006869
Publication No. US20030082166A1
GENERAL INFORMATION:
APPLICANT: Byaschuk, Orest w.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour. Barbara J.
ITILE OF INVENTION: COMPCOUNDS AND METHODS FOR MODULATING NONCLASSICAL
ITILE OF INVENTION: CADIBERIN MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-10-395-032-4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

S9.5%; Score 25; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.1%; Score 24; DB 14; Length 7; 42.9%; Pred. No. 1.2e+06; vative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-10-006-869-3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-006-869-3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Search completed: September 5, 2004, 11:24:05 Job time : 67 secs
                   1 CDPVSGC 7
1 CVPLTSC
                      g
```

0;

Gaps

·;

This Page Blank (uspto)

```
Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|: ||
CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; MOLECULE TYPE:
US-08-526-710-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 1375, Ap
Sequence 1371, Ap
Sequence 1371, Ap
Sequence 3971, Ap
Sequence 3971, Ap
Sequence 371, Ap
Sequence 371, Ap
Sequence 1371, Ap
Sequence 1374, Ap
Sequence 1374, Ap
Sequence 2174, Ap
Sequence 2174, Ap
Sequence 2155, Ap
                                                                      5, 2004, 11:16:10 ; Search time 21 Seconds (without alignments) 17:209 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-526-710-21
US-09-226-955-21
US-09-227-906-21
US-09-187-859-1375
US-09-187-859-1375
US-09-187-859-1375
US-09-187-859-1375
US-09-187-859-3971
US-09-187-859-3971
US-09-187-859-3971
US-09-839-5428-3574
US-09-839-5428-3574
US-09-187-859-1740
US-09-187-859-1740
US-09-187-859-1740
US-09-187-859-1392
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                              389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                     US-09-761-636A-11
42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                               1 CVPLTSC 7
                                                                       September
                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                                                                                                                                                                                                                                                                                12645
                                                                                                                     Title:
Perfect score:
                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                  Database
                                                                       Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
```

1, Ap Appl Appl Appl Appl Appl Appl Appl A		
APP		
4041 1826 435, 435, 726, 726, 726, 73621, 73621, 73621, 73621, 73621, 73621, 73621, 73621, 73621, 73621, 73621,		
sequence seq		
		ų
		That
		lles 'Vivo
1. 8008		25 oc
204 200 200 200 200 200 200 200 200 200		#1.
28-4 28-4 28-4 28-4 38-7 652-4 38-7 28-2 29-3 29-3 28-3 28-3 28-3 28-3 28-3 28-3 28-3 28		
- 8522 - 9524 - 9652 -	NTS	tifying sted Org
- 639 - 639 - 639 - 629 - 639 - 633 - 633	ALIGNMENT	dentify slected brive, 0, Ver 710
3.0 0 0 D D C 0 0 0 0 0 0 0 0 0 0 0 0 0 0	LIG	.0 .0, .710 .771
US-09	ď	7.5 ET 2.5 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1
		10-21  21, Application US/08526710  1. S622699  ANT: Ruoslahti, Erkki ANT: Pasqualini, Renata OF INVENTION: Method of Ide OF SEQUENCES: 44  FONDENCE ADDRESS: 44  FONDENCE ADDRE
4 4 2 4 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		SE   SE   SE   SE   SE   SE   SE   SE
C ひ 母 母 母 C C C C C C C C C C C C C C C		Application US/085 22569 RAMATION: RAMATION: RAMATION: Pacqualini, Rena VENTION: Method VENTION: Method VENTION: Home to SEQUENCES: 44 A370 La Jolla Vil an Diego A170 La Jolla Vil an Diego A170 La Jolla Vil an Diego A2 La A370 La Jolla Vil A170 La Jolla
		pplication 2569 WATION: Ruoslahti, Paggualini VENTION: MUEADLES: NCE ADDRESS: NCE A
00 00 <del>4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4</del>		pplicat: 699   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569   569
552 572 572 572 572 572		Application 222699 NEMATION: Rucelaht Pasquali NVENTION: NVENTION: SEQUENCES: SEQUENCES: OBJOINT DATA A370 La J A470
		110-21 21, Application Secretary and application of INFORMATION: OF INVENTION: OF INVENTION: OF SEQUENCES SERVED ADDR. SESSEE: Campb. EET: 4370 La. Sen Diego. SESSEE: Campb. EET: 4370 La. Sen Diego. TRY: United: 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 92122 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222 9222
222222222222222222222222222222222222222		110 21, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50- 11, 50-
8 0 0 1 2 E 4 10 6 C E 6 C = 2 C E 4 10		SULT 1 -08-526- Sequence Patent Netering APPLIC COMPUT STAM STAM STAM APPLIC COMPUT COMPUT COMPUT FILLI F
2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT CONTRACTOR OF CONTRACTO
		AD

·,

Gaps

. 0

73.8%; Score 31; DB 1; Length 7; 57.1%; Pred. No. 3e+05; 1; Indels 1; Indels

```
Query Match
Best Local Similarity 57.13
Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 7 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-226-985-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:|: ||
1 CLPVASC 7
                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-227-906-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rucellahri, Erkki
APPLICANT: Rucellahri, Renata
TITLE OF INVENTION: Molecules That Home to a Selected Organ In Vivo
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                              GENERAL INFORMATION:
APPLICANT: Rucelahti, Brkki
APPLICANT: Rucelahti, Brkki
APPLICANT: Rucelahti, Rendat
APPLICANT: Pasqualini, Rendat
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Method of Selected Organ In Vivo
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUWTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
                                                                                                                                                                                                                                                                                                                                                                CAPPTER FEADABLE FORM:

MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: Ploppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,855
FILING DATE:
CLASSIFICATION NUMBER: US/08/862,855
FILING DATE: 11-SEP-1995
FILING DATE: 11-SEP-1995
FILING DATE: 10-SEP-1995
FILING DATE: 10-MARA-1997
FILING DATE: 10-MARA-1997
FILING DATE: 10-MARA-1997
ATTORNEY/AGRNT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 9-LJ 2621
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 21:
SEQUIENCE CHARACTER LSTICS:
LEMMENT 7 AMILY ACHIEFA: 7 AMILY ACHIEFA: 7 AMILY ACHIEFA: 10-SEQ ID NO: 21:
SEQUIENCE CHARACTER SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31; DB 3;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/09226985
Patent No. 6296832
GENERAL INFORMATION:
                                  ; Sequence 21, Application US/08862855
; Patent No. 6068829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4370 La Jolla VCITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 7 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-862-855-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|: ||
1 CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-226-985-21
RESULT 2
US-08-862-855-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
WEDIUM TVEE, Frompt tibe

COUNTRY OF STRING STRING COMPANIANCE COMPANIANCE STRING STRI
```

.. 0 . 0

Gaps

. 0

```
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052.
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3971, Application US/09187859A

Patent No. 6359820

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407c1
CURRENT FAPLICATION WHOBER: US/09/187,859A

CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                        ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence US-09-839-542B-1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-09-187-859-3971
                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                      Score 26; DB 4; Length 7;
Pred. No. 3e+05;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.5%; Score 25; DB 4; Length 7; Best Local Similarity 57.1%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1799, Application US/09187859A Patent No. 6358920 GENERAL INFORMATION:
                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                 h 61.9%;
Similarity 57.1%;
4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                  1 CVPLTSC
                                                                                                                                                                                                                                                                                                                                                                                                1 CEPKTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-187-859-1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-187-859-1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-187-859-3971
                                       SEQ ID NO 1375
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3971
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-839-542B-1375

J Sequence 1375, Application US/09839542B

J Batent No. 6569996

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Symonds, James Matthew

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS

TITLE OF TWENTON: 100006 407D1

CURRENT APPLICATION NUMBER: US/09/839,542B

CURRENT PILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPENIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C1
CURRENT APPLICATION WUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-7 cell adhesion recognition sequence US-09-187-859-1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.9%; Score 26; DB 4; Length 7; 57.1%; Pred. No. 3e+05; 3: Indels ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31; DB 4;
Pred. No. 3e+05;
2; Mismatches
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/862,855
FILING DATE: 23-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR EQO ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1375, Application US/09187859A Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                                                 73.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                      LENGTH: 7 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-227-906-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|: ||
1 CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ČEPKTGĆ 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CVPLTSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-09-187-859-1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

.; 0

Gaps

.

```
CDPKTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-187-859-3574
                                        US-09-839-542B-3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1799, Application US/09839542B
; Sequence 1799, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOINDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOINDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOINDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOINDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOST, 40701
CURRENT FILING DATE: 2001.04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIN Ver. 2.0
; SECTUMARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                        Gaps
                                                                                                                                                                                                                         Sequence 4047, Application US/09187859A
Sequence 4047, Application US/09187859A
Refent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-09-839-5428-1799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .<del>.</del>
                                            .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 7;
Score 25; DB 4; Length 7; Pred. No. 3e+05;
                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.5%; Score 25; DB 4; Best Local Similarity 57.1%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
  59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1.
                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CDPKTGC 7
  Query Match
Best Local Similarity
                                                                                       1 CVPLTSC 7
                                                                                                                               1 CDPKTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-839-542B-1799
                                                                                                                                                                                                RESULT 9
US-09-187-859-4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-187-859-4047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4047
                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                         à
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
Sequence 3971, Application US/09839542B
; Sequence 3971, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN. MEDIATED FUNCTIONS
TITLE OF INVENTION: CAPHERIN. MEDIATED FUNCTIONS
TITLE OF INVENTION: CAPHERIN. MEDIATED
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3971
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Blaschuk.

APPLICANT: Blaschuk.

APPLICANT: Gour, Barbara J.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: CADHENIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407D1

CURRENT APPLICATION NUMBER: US/09/839,542B

CURRENT FILING DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-09-839-542B-4047
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-09-839-542B-3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 4; Length 7; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 4; Length 7; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 35.4, Application US/09187859A; Patent No. 6358920; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.5%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDPKTGC 7
```

```
FITLE OF INVENTION: and Analogs Thereof to Birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: September 5, 2004, 11:19:28
Job time : 22 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-947-035-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   °.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                  APPLICANT: GOLY, BATCH J. T. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 1000066.4070.1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998:11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blaschuk, Orest W. APPLICANT: Blaschuk, Orest W. APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Gour, Barbara J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS FILE REFERENCE: 100086.407D1 CURRENT APPLICATION NUMBER: US/09/839,542B CURRENT FILING DATE: 2001-04-20 NUMBER OF SEQ ID NOS: 4052 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3574 LENGTH: 7
                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion US-09-187-859-3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Representative cyclic modulating agent based on a OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion CTHER INFORMATION: recognition sequence US-09-839-542B-3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Francis, Geoffrey L.
APPLICANT: Walton, Paul E.
APPLICANT: Ballard, Francis J.
APPLICANT: Amurty, John P.
APPLICANT: Phelps, Patricia V.
TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24; DB 4; Length 7;
Pred. No. 3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.1%; Score 24; DB 4;
42.9%; Pred. No. 3e+05;
ative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3574, Application US/09839542B Patent No. 6569996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/07947035
Patent No. 5444045
GENERAL INFORMATION:
APPLICANT: Francis, Geoffrey L.
APPLICANT: Walton, Paul E.
APPLICANT: Malton, Paul E.
APPLICANT: Malton, Paul E.
APPLICANT: Phelps, Patricia V.
APPLICANT: Phelps, Patricia V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%;
                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
APPLICANT: Blaschuk, Orest W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:: |
CDPVSGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CDPVSGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-839-542B-3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-947-035-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
```

ó

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.8%; Score 23; DB 1; Length 6; 80.0%; Pred. No. 3e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                  COUNTRY: U.ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,035
FILING DATE: 17-SEP-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5175-59
TELECOMMUNICATION INFORMATION:
TOWNS INFORMATIO
                                                                                                                                                         STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 5444045th Carolina
COUNTRY: US
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0%;
As 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
```

This Page Blank (uspto)

```
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
```

OM protein - protein search, using sw model

September Run on:

5, 2004, 11:22:56; Search time 21 Seconds (without alignments) 27.483 Million cell updates/sec

US-09-761-636A-12

1 CVPLTC 6 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

316 Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 6 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARTES

		₩			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length	DB	ΩI	Description
ч		N	r	7	B22565	R-phycoerythrin al
2	15	39.5	9	~	I65546	_
æ		9	S	7	E60274	
4		9	5	7	F22565	
Ŋ	14	36.8	9	N	149421	laminin B1 - weste
9	11	28.9	4	N	A32039	ela
7	11	28.9	4	7	154357	schwannomin - mous
00	11	28.9	ហ	7	A60521	С
σ	11	28.9	9	Ŋ	137263	Y protein - human
10	11	28.9	9	C)	H48394	glycoprofein compo
11	10	26.3	9	N	C22565	R-phycoerythrin he
12	6		m	m	A22565	R-phycoerythrin al
13	თ	23.7	4	7	I51049	٠,
14	σ	-	4	~	843959	Id mu chain V regi
15	σ		4,	N	S55238	pallidipin - assas
	σ		S	~	A33882	di
17	σ		S	N	B37988	4~
18	6	23.7	Ŋ	N	B45525	actin I - malaria
19	σ	23.7	വ	7	S65726	lobin
20	6	23.7	5	7	S11127	phosphoprotein, bo
21	6	23.7	9	7	A61049	
22	6	23.7	φ	~	JU0355	33
23	6	23.7	φ	7	PQ0008	- 1
	σ	23.7	9	7	A27696	contraction-inhibi
	σ	23.7	9	~	B27696	contraction-inhibi
	σ		9	~	137027	protamine P1 - dor
	6	•	9	7	I67345	MHC H2-K-k Gell Su
28	9	23.7	9	~	PT0652	
29	σ	23.7	9	N	F41946	T-cell receptor ga

Na+/K+-exchanging	hypothetical TCL3	tyrosine protein k	proctolin - Americ	peptidyl-dipentida	peptidyl-dipeptida	flagellar protein	andiotensin-conver	proctolin - Atlant	hypothetical prote	hypothetical colla		1	thyroliberin - she	ı	rel
S29881	179564	I78890	HOROHA	JN0862	JN0860	E42364	PQ0009	A60411	\$53595	A35039	RHTDTO	RHPGT	RHSHT	A92971	A33802
8	4	ю	-1	N	~	7	~	7	~	4	m	m	٣	е	m
9	9	٣	ß	Ŋ	Ŋ	Ŋ	Ŋ	ß	S	9	3	e	m	٣	3
23.7	23.7	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	21.1	18.4	18.4	18.4	18.4	18.4
Q	σ	œ	80	80	80	80	00	œ	œ	œ	7	7	7	7	7
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

ч	
₽	L
ы	•
₽	L
S	c
f-1	-

RESULT 1
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Recession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Gaps ., 52.6%; Score 20; DB 2; Length 5; 100.0%; Pred. No. 2.8e+05; ive 0; Mismatches 0; Indels Query Match 52.6 Best Local Similarity 100. Matches 3; Conservative

.. 0

1 CVP 3 2 CVP 4 ò g

Enhancer-like sequences and thei RESULT 2
166546
MHC H2-L antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 165546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1986
A,Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequen A,Reference number: 152778; MUID:86106202; PMID:3510743
A;Reference number: 155546
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>

A; Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

. 0 Query Match 39.5%; Score 15; DB 2; Length 6; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 1; Indels

0

Gaps

S 2 VPCT g ò

RESULT 3 E60274 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment) C;Species: Mycobacterium tuberculosis

0;

```
schwannomin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I54357
R;Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A;Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are con A;Reference number: I54357; MUID:95072570; PMID:7981675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N.Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muschafterence number: A60521, MUID:90227907; PMID:2109669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 1-5 <BON>
C;Superfamily: glucan phosphorylase
C;Reywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
C;Accession: A32039
R;Horvath, A.; Kastin, A.J.
B;Horvath, A.; Kastin, A.J.
B;Horvath, A.; Kastin, A.J.
B;Horvath, A.; Kastin, A.J.
B;Horvath, A.; Kastin, A.J.
A;Horvath, A.; Esclation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor A;Reference number: A32039; MUID:89123285; PMID:2563371
A;Recession: A32039
A;Roceosion: A32039
A;Residues: 1-4 cAROx
A;Residues: 1-4 cAROx
A;Residues: Lye carox
C;Superrimental source: brain
C;Superrimental source: brain
C;Superrimental source: brain
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923
A;Genetics:
A;Gene: NF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

28.9%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                           Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4;
                                                                                                                                                                                                                                                                                                                                                      28.9%; Score 11; DB 2; Le 100.0%; Pred. No. 2.8e+05; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11; DB 2; Lo
Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 28.9%; Score 11; DB Similarity 100.0%; Pred. No. 2.6 2; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.1
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
A60521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: I49421 F. Forton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H. R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H. Ammun. Genome 5, 349-355, 1994 A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR. A;Reference number: I48934; MUID:94319082; PMID:8043949
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: E60274
A;Accession: E60274
A;Accession: preliminary
A;Residues: 1-5 <NAG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment) C,Species: Gastroclonium coulteri C,Species: Gastroclonium coulteri C,Species: Or-Mar-1988 #text_change 23-Mar-1993 C,Accesion: F22565 C,Accesion: F22565 R,Klotz, A.V.; Glazer, A.N. A.Title: Characterization of the bilin attachment sites in R-phycoerythrin. A,Reference number: A22565, MUID:85182601; PMID:3886644 A,Accesion: F22565 A,Molecule type: protein A,Residues: 1-5 <KLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taminin Bl - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: 149421
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: 10A
A,Residues: 1-6 <RES>
A,Cross-references: EMBL:U05736; NID:9497073; PIDN:AAB60477.1; PID:9642829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.8%; Score 14; DB 2; Length 6; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           36.8%; Score 14; DB 2; Length 5; 66.7%; Pred. No. 2.8e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.8%; Score 14; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ):|
3 PIT 5
                                                                                                                                                                                                                                                                                                                                                                                                                             3 PLT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ဥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

ö

ö

S

ζ

g

```
×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cydocession: IS1049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Bur. J. Blochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) A;Reference number: IS1049; MUID:95324545; PMID:7601121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 10-0ct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43959
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, I Mucleic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice. A;Reference number: S43956; MUID:94248036; PMID:8190629
                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-4 <OLS>
A,Residues: 1-4 <OLS>
A,Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
                                                                                                                                                                                                                                                                       red alga (Gastroclonium coulteri) (fragment)
                                                                                                                                                                                                                                                                                           Cippecies: Gastroclonium coulteri
Cipate: 15-Unn-2001 #sequence_revision 15-Unn-2001 #text_change 15-Jun-2001
CiAccession: A22565
FixIotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A.Fitle: Characterization of the bilin attachment sites in R-phycoerythrin.
A.Reference number: A22565; MUID:85182601; PMID:3886644
A.Accession: A22565
A.Molecule type: protein
A.Residues: 1-3 <KLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%; Score 9; DB 3; Length 3; 100.0%; Pred. No. 2.8e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.7%; Score 9; DB 2; Length 4;
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.7%; Score 9; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05;
Pred. No. 2.8e+05;
1; Mismatches 0;
Similarity 50.0%;
1; Conservative
                                                                                                                                                                                                                                                                       R-phycoerythrin alpha-1 chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-4 <WAG>
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1; Conserva
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                              CL 5
                                                                            1 CV 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 C 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              о-
С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                843959
                                                                                                                         g
                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                     Y protein - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Now-sapiens (man)
C.Saccession: 137263
E.MacDer, G., Habener J.F.
Endocrinology 131, 2010-2015, 1992
A.Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna A.Reference number: 137263; MUID: 93010691; PMID: 136344
A.Reference number: ranslated from GB/EMBL/DDBJ
A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (from Cispecies: Bos primigenius taurus (cattle)
C;Species: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: #48394
R;Mather, 1.H.; Banghart, L.R.; Lane, W.S.
R;Mather, 1.H.; Banghart, L.R.; Lane, W.S.
A;Hitle: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Gastroclonium coulter:
C.Species: Gastroclonium coulter:
C.Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C.SAccession: C25565
R.Kidotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A.Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A.Reference number: A22565; MUID:85182601; PMID:3886644
                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-6 <RESS>
A;Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
```

1; Indels Length 6;

Score 11; DB 2; ]
Pred. No. 2.8e+05;
0; Mismatches 1

28.9%;

2; Conservative

9

qq à

Best Local Similarity Matches 2: Conserv

Query Match

A;Note: sequence extracted from NCBI backbone (NCBIP:131518) C;Keywords: glycoprotein

A; Experimental source: milk A; Molecule type: protein A; Residues: 1-6 < MAT>

A;Status: preliminary

A;Reference number: A48394; MUID:93250576; PMID:8485470 A;Accession: H48394

DB 2; Length 6;

26.3%; Score 10;

A;Molecule type: protein A;Residues: 1-6 <KLO>

Query Match

1; Indels

28.9%; Score 11; DB 2; Length 6; 66.7%; Pred. No. 2.8e+05; ive 0; Mismatches 1; Indels

Conservative

Best_Local Similarity Matches 2; Conserv

ð Dp

Query Match

A; Gene: CREB

a e

0;

0; Gaps

0; Indels

0; Mismatches

1; Conservative

Matches

```
PESULT 15

RESULT 15

S5528

pallidipin - assassin bug (fragment)
C;Species: Triatoma pallidipennis (assassin bug)
C;Species: Triatoma pallidipennis (assassin bug)
C;Species: Triatoma pallidipennis (assassin bug)
C;Date: 19-Mar-1997 #sequence_revision 18-Uul-1997 #text_change 19-May-2000
C;Date: 19-Mar-1997 #sequence_revision 18-Uul-1997 #text_change 19-May-2000
C;Caccession: S5528
R;Haendler, B: Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin Biochem. J. 307, 465-470, 1995
A;Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib A;Reference number: S55238; MUID:95251610; PMID:7733884
A;Accession: S55238
A;Accession: S552
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

5, 2004, 11:19:31; Search time 15 Seconds (without alignments) 20.828 Million cell updates/sec September on: Run

US-09-761-636A-12 38 Perfect score:

1 CVPLTC 6

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

50 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 6

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	711 eitoti 2000 die de	herren	litoria		mytilia	nerinlan		_	pseu	P36515 saccharomyc		citro					leptino	P41495 sarcophaga		litoria	litoria	clostrid		hirud		anthop		_	4 canie f	703 4	A DYNOTO DA	٠.	9	
SUMMARIES		EIO1 LITRU		EI03_LITRU	CIP1 MYTED	CIP2 MYTED	PRCT PERAM		THYL_PIG		RM01 YEAST	TUFT HUMAN	BIOA_CITFR	BPP7 BOTIN	EI04_LITRU		SUGA_ACHDO		TMOF_SARBU		RE31_LITRU		UN06_CLOPA	EOSI HUMAN	FAR3_HIRME	FLRF HIRME	FLRN ANTEL		RE11 LITRU	TPIS CANFA	UC22 MAIZE	ACPH_RABIT	LUXE_VIBFI	FYRI_ANTEL	
	Length DB	1						6					2 1						6 1															4 1	
de	Query Match	34.2	28.9	23.7	23.7	23.7	21.1	21.1	18.4	18.4	<b>x</b> 0	m o	18.4	20 0	o o	18.4	σ.	æ	18.4	٠. س	ë,	ش	13.2		· .		<i>.</i>	٥.	Ö						
	Score	13	11	6	6	6	<b>6</b> 0	<b>c</b> o :	7	- 1	٦ ~	~ [	٦ -	٦ /	۱ ~	7		7	7	υı	in I	ıΩ	Λ.	4' ~	4 •	4.	4, ,	4.	4	4	4	4	m	e	
	Result No.	7	7	m	4	Ŋ	9	7	œ «	י ע	7.	1 5	7.5	L L	# L	77	9 I	17	18	910	0 70	77	7 6	2.0	# u	670	9 10	7 7	870	67	30	31	32	3.3	

P41853 artioposthi P82071 litoria rub P38639 mus musculu P19918 pseudomonas P42563 hirudo medi P01162 macrocallis P12997 citrobacter P58649 octopus min P38005 chlamydia t P41491 locusta mig P01157 homo sapien P35904 achatina fu		4. 0	pdate) Vertebrata, Euteleostomi, a; Hyloidea, Hylidae;	Wallace J.C.; Australian buzzing tree frog skin peptides from Litoria	CRC64;	1); Length 6; e+05; 0; Indels 0; Gaps 0;		6 AA.  date) update) tein (virion protein UL38)  KOS).  Herpesviridae;  e M., Hecht L.B.,  type 1 promoter controlling the
5 1 FARP ARTTR 5 1 UF01_MOUSE 6 1 UF01_MOUSE 6 1 DCMS PSECH 6 1 FARQ—HIRME 7 1 FARQ—HIRME 7 1 FARG—MOUI 7 1 LOCAT 7	ALIGNMENTS	PRT; eated) st sequence up	st annotation u .ree frog). .ata; Craniata; .a; Neobatrachi	Tyler M.J., glands of the son with the	. 52:639-645(1999). AR LOCATION: Secreted. BCIFICITY: Skin. ense peptide; Amidation. AMIDATION. AAI 792 MW; 6683704772C9A000 CRC64	14.2%; Score 13; DB 16.7%; Pred. No. 1.4 .ve 1; Mismatches		T; 6 AAnce update) ation update) ation update)
33.43 33.45 33.47 33.47 33.47 33.47 33.47 33.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47 34.47		LT 1 LITRU E101 LITRU S' P81096, 28-PEB-2003 (Rel 28-PEB-2003 (Rel	Locut-2003 (kel. 42, bar Electrin 1. Litoria rubella (Desert of Eukaryota; Metazoa; Choro Amphibia; Batrachia; Anu Pelodryadinae; Litoria. NCBI TaxID=104895;	SEQUENCE. TISSUE=Skin secre Wabnitz P.A., Bow "Peptides from the Litori electrica.	AUST. J. Chem. 52:639-645(1999) -1- SUBCELLULAR LOCATION: Secre -1- TISSUE SPECIFYCITY: Skin. Amphibian defense peptide; Amid MOD_RES 6 6 A SEQÜENCE 6 AA; 792 MW; 6683	ry Match t Local Simil ches 2; C	2 VEL 4 	SVIK P19 HSVIK 23210, 23210, 23210, 1-NOV-1991 (Re 1-NOV-1991 (Re 5-MAR-2004 (Re spend a protein L38. L38 inplex iruses; dsDNA. Iphaherpesviri CDI TaxID=10108 BDLINE=9110128 HBARAGAN NM., Ilverstein S., Analysis of th
		50.0	00000000000000000000000000000000000000			Que Bes Mat	· 음	RESULT VP19 H VP VP19 H VP

ö

0

```
TISSUB-Pedal ganglion;
MEDLINE-88240357; PubMed=3377776;
MEDLINE-88240357; PubMed=3377776;
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
Hirata T., Kubota I., Iwasawa Mytilus inhibitory peptides.";
"Structures and actions of Mytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
                                                                                             TISSUE=Pedal ganglion;
MEDLINE=88240357; PubMed=3377776;
MEDLINE=88240357; PubMed=3377776;
MINIATE T., KLUDOCA I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
"Structures and actions of Mytlius inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
-:- FUNCTION: Inhibitory action on contractions in several molluscan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide II (MIP II).
Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea, Mytilidae; Mytilus.
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                               Score 9; DB 1; Length 6;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 9; DB 1; Length 6; Pred. No. 1.4e+05; 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AA; 621 MW; 72C9C6876DD81000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Periplaneta americana (American cockroach), Limulus polyphemus (Atlantic horseshoe crab), and
                                                                                                                                                                                                                                                                             AMIDATION.
72C9C68775B81000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION
             Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                   23.7%;
                                                                                                                                                                                                                  -!- SIMILARITY: TO MIP II. PIR, A27696; A27696. Hormone, Amidation. MOD_RES 6 6
                                                                                                                                                                                                                                                                                                6 AA; 637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO MIP I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B27696; B27696.
Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (
21-JUL-1986 (
01-FEB-1995 (
                                                                                                                                                                                                                                                                                                                                                                                                               3 PL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proctolin.
                                                                                                                                                                                                               muscles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRCT PER
P01373;
                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESULT 5
CIP2_MYTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRCT_PERAM
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                TYPICE SET 169-786 (1991).

-I- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.

-I- SIMILARITY: Belongs to the herpesviruses VP19C family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., "reptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
           expression of UL18, a true late gene involved in capsid assembly.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.7%; Score 9; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;
                                                                                                                                                                                                                                                                                                              6 AA; 703 MW; 67376451A336F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                               DB 1; Le . 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Ontraction-inhibiting peptide I (MIP I).
Mytilus edulis (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA.
                                                                                                                                                                                                                                                                                     Capsid assembly; Coat protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                           Query Match

28.9%; Score 11; DB

Best Local Similarity 100.0%; Pred. No. 1.4

Matches 2; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rubella.";
Aust. J. Chem. 52:639-645(1999).
-- SUBCELLUJAR LOCATION: Secreted.
-- SUBCELLUJAR LOCATION: Skin.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Litoria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                          EMBL; M57646; AAA45830.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rissum=Skin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PM 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIP1 MYTED P13736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EI03 LITRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Electrin 3
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P82099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIP1_MYTED
```

EI03_LITRU

d

à

ô

Gaps

٠,

0; Indels

RESULT

g

ID DT DT DT OS

```
MEDLINE=89335826; PubMed=2503057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=Pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THYL PIG
P01151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNTHESIS
                                                                                 putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THYL PIG
                       RAME SOUND DESCRIPTION OF THE SECOND OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                     SPECIES=P.americana;
MEDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional regulator trpl (TrpBA operon transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stangier J., Dircksen H., Keller R.,
"Identification and immunocytochemical localization of proctolin in
Peptidatal organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81225865; PubMed=6113690; O'Shea M., Adams M.E.; "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Stimulates cardiac output and hindgut motility, modulates visceral and skeletal muscle in many arthropods.
-!- TISSUE SPECIFICITY: Found in the lateral white neurons and in the crab pericardial organs.
PIR; A01644; HORCHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Identification of proctolin in the central nervous system of
                       Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blattoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-L.polyphemus;
MEDLINE=90287800; PubMed=2356151;
Groome J.R., Tillinghast B.K., Townley M.A., Vetrovs A., Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.1%; Score 8; DB 1; Length 5; 50.0%; Pred. No. 1.46+05; ive 1; Mismatches 0; Indel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA; 649 MW; 71B7673B44600000 CRC64;
    maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 horseshoe crab, Limilus polyphemus.";
Peptides 11:205-211(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=C.maenas;
MEDLINE=86232789; PubMed=2872661;
                                                                   Blattidae, Periplaneta.
NCBI_TaxID=6978, 6850, 6759;
                                                                                                                                                                                                                                                                     Life Sci. 17:1253-1256(1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activator) (Fragment).
                                                                                                                                                                                                                                                                                                                                      SPECIES=P.americana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                    BIOLOGICAL SOURCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-PPG1 C1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRPI PSEPU P36414;
                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRPI_PSEPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ward D.N.; "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE=703, MEDILINE=703, PubMed=4982117; Bowers C.Y., Schally A.V.; Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.; "The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutamyl-histidyl-proline amide."; Biochem. Biochem. Biochem. 37:705-710(1969).
                                                                                                                      Biochimie 71:521-531(1989).

-!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHAGE SUBDINTS: IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL POSEMATE), TRP1 BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

-!- SIMILARITY: Contains 1 HTH 1yer-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombina orientalis (Oriental fire-bellied toad), and Notophthalmus viridescens (Eastern newt) (Triturus viridescens). Eukaryota; Metazoa; Chordata; Craniata; Verebrata; Eutheria; Catartiodactyla; Suina; Sutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FBD-2003 (Rel. 41, Last annotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
Sus scrofa (Pig),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=Sheep; TISSUE=Hypothalamus;
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
Eberly L., Crawford I.P.;
"DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tryptophan biosynthesis; Transcription regulation; Activator; DONA principle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=Pig; TISSUB=Hypothalamus;
MEDLINE=70136150; PubMed=4984938;
Nair R.M.G., Barrett J.E., Bowers C.Y., Schally A.V.;
"Structure of porcine thyrotropin releasing hormone.";
Biochemistry 9:1103-1106(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Score 8; DB 1; Le 50.0%; Pred. No. 1.4e+05; Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000847; HTH LYSR.
PROSITE; PS50931; HTH LYSR; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X13299; CAA31660.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCOOS ON THE BEACT OF THE BEACT ON THE BEACT OF THE BEAC
```

ö

·: 0

Gaps

÷

SYNTHESIS

SEQUENCE

SEQUENCE

```
SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91285106; PubMed=2060626;
Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; FEBS Lett. 284:51-56(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YmLl) (Fragment)
                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
                                                                                                                              18.4%; Score 7; DB 1; Length 4; 100.0%; Pred. No. 1.4e+05; iive 0; Mismatches 0; Indeli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AA; 402 MW; 7771B2D5D000000 CRC64;
                                                                                           SEQUENCE 4 AA; 441 MW; 7761E876F000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 18.4%; Score 7; DB 1; Lei Local Similarity 100.0%; Pred. No. 1.4e+05; nes 1; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                        4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=72187087; PubMed=4112769;
                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosomal protein; Mitochondrion.
                                          PIR; PL0140; PL0140.
Oxidoreductase; Molybdenum.
NON TER 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                          1; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
IMMUNOGLOBULIN CLASS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S17255; S17255.
SGD; L0002681; MRPL1
                                                                                                                                 Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Э
Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitakawa M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 P 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUFT HUMAN
                                                                                                                                                                                                              3
P
                                                                                                                                                                                                                                                                                                                                            RM01 YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01858;
                                                                                                                                                                                                                                                                                                                                                           P36515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
TUFT HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                         RM01_YEAST
                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
               SPER
                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Neurochem. 23:471-478(1974).

-i. FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/ neuromodulator in the central and peripheral nervous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of Co dehydrogenase structural genes in
carboxydotrophic bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arch. Microbiol. 152:335-341 (1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=N.viridescens,
MEDLINE=75035605, PubMed=4214528;
Grimm-Joergensen Y., McKelvy J.F.;
Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ပ္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales;
Bradyrhizobiaceae.
                                                                                                                                                                                                                                                        SPECTES=B.orientalis; TISSUE=Skin; MEDLINE=76138399; PubMed=815011; Ashuhara T., Nakajima T.; Nakajima T.; Nakajima T.; Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin."; Chem. Pharm. Bull. 23:3301-3303(1975).
                                                                                       SPECIES=Sheep;
MEDLINE=70163386; PubMed=4985794;
Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
Guillemin R.;
"Characterization of ovine hypothalamic hypophysiotropic
TSH-releasing factor.";
Nature 226:321-325(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neuromognia...
pIR, A9019; RHTDTO.
PIR; A92971; A92971.
PIR; A93750; RHSHT.
Amidation; Pyrrolidone carboxylic acid.
1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P19916;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.4%; Score 7; DB 1; Length 3; 100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 380 MW; 7761F6B00000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ı- COFACTOR: Molybdenum (molybdopterin)
                     spectrometry.";
Org. Mass Spectrom. 5:221-228(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=90055678; PubMed=2818128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas carboxydohydrogena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               е
Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 P 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dioxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCML PSECH
P19916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
```

DCML_PSECH

RESULT 9

Matches

ò 셤

ó

Gaps

.. 0

```
Query Match
Best Local Similarity
                                                                              2
                                                                              4 LT
                                                                                                                                                                           BPP7 BOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EI04 LITRU
P82100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - գ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electrin 4.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rubella."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
                                                                                                                                                                                       P30425;
                                                                                                                                                              BPP7_BOTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
EI04 LITRU
                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                            ਨੇ
                                                                                                      g
                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
           Fidalgo B.V., Najjar V.A.;

"The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";

Biochemistry 6:3386-3392(1967).

-! MISCELLANBOUG: An IGG (called leucokinin) binds reversibly to the cell membrane of neutrophils in the blood. Leucokininase on the membrane releases the active peptide tuftsin from the gamma chain. Tuftsin is essential for maximum stimulation of the phagocytic activity of neutrophils.

MIM; 191150; -.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii, and Salmonella typhimurium biotin operons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
-!- SIMILAHITY: Belongs to class-III of pyridoxal-phosphate-dependent
aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Citrobacter.
                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                        DB 1; Length 4;
                                                                                                                                                                             GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006909; P:phagocytosis; NAS.
SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR005814, Aminotrans 3.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AA; 582 MW; 6AAABIBIA6F00000 CRC64;
                                                                                                                                                                                                                                       Score 7; DB 1; Ler
Pred. No. 1.4e+05;
                                                                                                                                                                                                                           18.4%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               5 AA
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M21922; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: Pyridoxal phosphate.
 MEDLINE=68091045; PubMed=4169272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aminotransferase) (Fragment)
                                                                                                                                                                                                                                                                 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67:203-211(1988)
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Citrobacter freundii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diaminononanoate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; 140697; 140697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=546;
                                                                                                                                                                                                                                                                                            3 P 3
                                                                                                                                                                                                                                                                                                                     m
                                                                                                                                                                                                                                                                                                                     3 P
                                                                                                                                                                                                                                                                                                                                                                                          CITFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          BIOA CIT
P13071;
                                                                                                                                                                                                                                                                                                                                                                            BIOA_CITFR
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene
g
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cintra A.C.O., Vietna C.A., Giglio J.R.,

"Primary structure and biological activity of bradykinin potentiating peptides from Bothrops insularis snake venom.",

J. Protein Chem. 9:221-227(1930).

-!- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bradykinin potentiating peptide S5,2 (5A) (Angiotensin-converting
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Australian buzzing tree frog
skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Litoria rubella (Desert tree frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; G37196, G37196.

Hypotensive agent; Pyrrolidone carboxylic acid.

MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SEQÜENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;
                                                                                                                                                                                                                                                                                                                                           Bothrops insularis (Island jararaca) (Queimada jararaca)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4e+05;
les 0; Indels
Score 7; DB 1; Length 5; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wallace J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                               5 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 7; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J.,
"Peptides from the skin glands of the
Litori electrica. Comparison with the
                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Scc..
100.0%; Prev
0; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom;
MEDLINE=90351557; PubMed=2386615;
                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
18.4%;
                                    Conservative
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                             enzyme inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8723;
```

```
TISSUE=87057369; PubMed=3782138;
TISSUE=87057369; PubMed=3782138;
TA Lazarovici P., Primor N., Loew L.M.;
Lazarovici P., Primor N., Loew L.M.;
Thurification and pore-forming activity of two hydrophobic
Ty purification and pore-forming activity of two hydrophobic
Ty marmoratus).";
The Biol. Chem. 261:16704-16713 (1986).
The PUNCTION: Exhibits unusual shark repellent and surfactant properties. Porms voltage-dependent, ion-permeable channels
Ty membranes. At high concentration causes cell membrane lysis.
The SUBURITY: Monomer. In aqueous solution exists as a tetramer.
The SUBURITY: Belongs to the pardaxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pardaxin II (PXII) (Fragment)
Pardachirus marmoratus (Red sea moses sole).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Percostei; Teleostei; Ruteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Soleoidei; Soleidae; Pardachirus.
NEL TAXID=31087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.4%; Score 7; DB 1; Length 5; ilarity 100.0%; Pred. No. 1.4e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                  0; Indels
                                                                                                                                      Query Match
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AA; 614 MW; 7769C9C9C8100000 CRC64;
Amphibian defense peptide; Amidation.

MOD RES 5 AMIDATION.

SRQÜENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                               4 LT 5
                                                                                                                                                                                                                                                                                                                                     2 IT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 P 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P81864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
PAP2_PARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  loxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE COURT STATE STATE SOURCE COURT STATE STATE SOURCE COURT STATE STATE SOURCE COURT STATE STATE SOURCE COURT STATE SOURCE COURT STATE STATE SOURCE COURT STATE STATE SOURCE COURT STATE STATE STATE STATE SOURCE COURT STATE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                            g
               数計器
                                                                                                                                                                                                                                                                                                          à
```

Search completed: September 5, 2004, 11:25:35 Job time : 16 secs

۵,

Ŋ

셤

Н

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 5, 2004, 11:22:21; Search time 58 Seconds (without alignments) 32.640 Million cell updates/sec Run on:

US-09-761-636A-12 38 1 CVPLTC 6 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 seqs, 315518202 residues Searched:

11 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

SPTREMBL_25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_plant:*
10: sp_plant:*
11: sp_virus:*
13: sp_vertebrate:* sp_unclassified:*
sp_rvirus:*
sp_bacteriap:* 7: 99: 10: 11: 12: 13: 14: 15: 17: Pred. No. is the number of regults predicted by chance to have a score greater than or equal to the score of the regult being printed, and is derived by analysis of the total score distribution.

sp archeap:*

SUMMARIES

Description	PB3308 gallus gall PB3569 sepia offic PB3373 bacillus ce PB3533 lactcobacill PB2181 spinacia ol PB2541 spinacia ol PB3568 sepia offic Q08433 rattus sp. Q99007 hordeum vul PB3570 sepia offic
DI	P83308 P83569 P83573 P83533 P82541 P82541 P82542 Q00433 Q99007 P83570
DB	13 2 2 2 10 10 10 10 10 5
% Query Match Length DB	<b>ᲘᲡᲡᲡᲡᲡᲡᲡᲥᲥᲡ</b> Ს
% Query Match	31.6 23.7 13.2 13.2 10.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5
Score	Ⴗ ႷჿჁჄჄჄჄჄჄჄႷႷႷႷႷႷ
Result No.	100 8 4 5 5 5 1 1 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1

ALIGNMENTS

```
(TrEMBLrel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                             NCBI TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
01-JUN-2000 (
01-JUN-2000 (
01-OCT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P82541
P82541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P82541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
   ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteomics 2:765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.; "High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0003 (TrEMBLrel. 24, Created)
01-000-2003 (TrEMBLrel. 24, Last sequence update)
01-000-2003 (TrEMBLrel. 24, Last sequence update)
01-000-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria, Firmicutes; Lactobacillales, Lactobacillus.
NGBI_TAXID=1625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 13.2%; Score 5; DB 2; Length 6; Local Similarity 100.0%; Pred. No. 1e+06; nes 1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                             88 kDa protein (Fragment).
Bacillus cereus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5;
                                                                                                                                                                                      01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               5 AA; 623 MW; 6B01AAA336F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%; SCOre 5; DB 2; L 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
9
                                                                                                                                                       S AA.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
STRAIN-NCIME 11796;
STRAIN-NCIME 11796;
Stromin N., Dowds B.C.A.;
Submitted (JUL-2001) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity 100.0%;
1; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DSM 20451;
PubMed=12112860;
                                               PI 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                            PL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ທ
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P82181
P82181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                            m
                                                                 Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                            P83073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P83533
                                                                                                                                                         P83073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
P8353
P8353
P8353
P8353
P8 525
P8 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                    RESULT 3
P83073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P82181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                           8
                              ò
```

```
Yamaguchi K., von Knoblauch K., Subramanian A.R.;

"The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 37:28455.28465(2000)

-! FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

-! SUBCELLULAR LOCATION: CHLOROPLAST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -: TISSUE SPECIFICITY: EXPRESED IN ALL PLANT TISSUES.
-: MASS SPECTROMETRY: MW=10477.0; MBTHOD=ELECTROSPRAY.
-: MASS SPECTROMETRY: MW=104977.0; MBTHOD=ELECTROSPRAY.
-: MASS SPECTROMETRY: MW=10495; MBTHOD=MALDI.
-: MISCELLANBOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA FORM IS THE MINOR BASIC FORM.
-: MISCELLANBOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
-: SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOWAL PROTEINS.
G0; G0:0009507; C:chloroplast; IEA.
G0; G0:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukarycta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 5; DB 10; Length 6;
100.0%; Pred. No. 1e+06;
cive 0; Mismatches 0; Indels
01-JUN-2000 (TrEMBLrel. 14, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Chloroplast 508 ribosomal protein L10 beta (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TremBlrel. 25, Last annotation update)
01-0CT-2003 (TremBlrel. 25, Last annotation (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, FUNCTION, AND MASS SPECTROMETRY. STRAIN=cv. ALWARO; TISSUE=Leaf; MEDLINE=20435797; PubMed=10874039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spinacia oleracea (Spinach)
Chloroplast.
                                                                                             Spinacia oleracea (Spinach)
```

. 0

```
SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                         TISSUE=Egg;
PubMed=10944467;
                                                                                                                                                                                                                                                                                                    TISSUE=Egg;
PubMed=12207899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 V 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            008433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               008433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               099007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
Q99007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    008433
                          REPRETATION OF SECOND SOLUTION OF SECOND SECOND SECOND SECOND SECOND SOLUTION SECOND S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC
DT
DT
DT
DT
DT
RR
RR
RR
RR
RR
DR
DR
DR
SQ
SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pheromone peptide Lime.
Sepia officinalis (Common cuttlefish).
Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinacia oleracea (Spinachi. Eubryophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
GO; GO:0003735; F:structural constituent of ribosome; IBA. InterPro; IPR002222; Ribosomal S19.
PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
Ribosomal protein; Chloroplast; rRNA-binding.
                                                                                                                                                                                              'Match 13.2%; Score 5; DB 10; Length 6; Local Similarity 100.0%; Pred. No. 1e+06; les 1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 gamma (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                            NON TER 6 6 S S SQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.2%; Score 5; DB 10;
100.0%; Pred. No. 1e+06;
ative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 T 5
                                                                                                                                                                                                                                                                                                                S
T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P82182
P82182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P83568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P83568
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P821823

P82 1821

P83 1821

P84 1821

P85 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
ZatyIny C., Gagnon J., Boucaud-Camou E., Henry J.;
"ILME: a waterborne pheromonal peptide released by the eggs of Sepia
officinalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                              STRAINS-Gunn;
MEDLINE-91282758; PubMed=1840486;
MEDLINE-91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic dunn rat.";
Blochem. Blophys. Res. Commun. 177:1161-1164 (1991).
EMBL; S38636; AAB19259.1;
GO: GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٠<u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%; Score 4; DB 5; Length 4;
100.0%; Pred. No. 1e+06;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.5%; Score 4; DB 11; Length 4; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                4 AA; 505 MW; 6B1697203000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1
4 AA; 473 MW; 633732C42000000 CRC64;
                                                                        Biochem. Biophys. Res. Commun. 275:217-222(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q99007;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
```

0;

·;

```
.<u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henry J., Favrel P., Boucaud-Camou E.;
Henry J., Favrel P., Boucaud-Camou E.;
"Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
"Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related
cuttlefish, Sepia officinalis.";
Peptides 18:1469-1474(1997).
-!- FUNCTION: REGULATORY NEUROREPTIDE WITH MYOTROPIC ACTIVITY
TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE COUDUCT
BY DECREASING TONUS, PREQUENCY AND AMPLITUDE OF CONTRACTIONS.
-!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.
GO: GO:0007218; P:neuropeptide signaling pathway; IEA.
Neuropeptide; Amidation.
MOD RES.
2 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                   Hordeum vulgare (Barley).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.

NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P83570;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last Bequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Neuropeptide GWa.
Sepia officinalis (Common cuttlefish)
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
                                                                                                                                                                                                                                                                                                                                               MEDITINE-91329704; PubMed=1831055;
Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic accid and abscisic acid in protoplasts prepared from mature bareley aleurone layers.";
Plant Mol. Biol. 16:713-721 (1991).
BMBL; X54643; CAA38455.1; -.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.3%; Score 2; DB 10; Length 5; Best Local Similarity 0.0%; Pred. No. 1e+06; Matches 0; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 0.0%; Score 0; DB 5; Length 2; Local Similarity 0.0%; Pred. No. 1e+06; les 0; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 2 AMIDATION.
2 AA; 261 MW; 737810000000000 CRC64;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                   Alpha amylase (Fragment).
AMY1 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Optic lobe;
PubMed=9437704;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 P 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 G 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ה
א יי
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 L 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P83570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
P83570
DD P8357
AC P8357
DD O1-JUJ
DD O1-JUJ
DD O1-JUJ
DD O1-JUJ
DD OC DECAP
OOC DECAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

Search completed: September 5, 2004, 11:26:39

Job time : 58 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

2004, 11:19:05 2, September Run on:

)5; Search time 62 Seconds (without alignments) 27.343 Million cell updates/sec

US-09-761-636A-12 38

Perfect score: Title:

1 CVPLTC 6 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

1586107 segs, 282547505 residues Searched:

of hits satisfying chosen parameters: Total number

59163

Minimum DB seq length: 0 Maximum DB seq length: 6

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* 2 M 4 G 9 C B Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

	Description	1			n e		۰ ۵	ח ת	n 1		ω,	д.	2 Fr	σ		σ	Aaw67428 HCV pepti	Aaw31456 Transcrip	Aay63235 Protocadh	7	N		٠,	v (	٥ ,	י עכ	<b>~</b>	Aay56095 Glycohaem
SUMMARIES	ID	AAU04531	AAY61488	AAV62223	AAV62763	AAY62006	AAY64259	AAY85373	AAV62757	AAVKOABB	ABY44431	4477	AAD40760	AAD77033	AAMO4450	AAMO440V	AAM6/428	AAW31456	AAY63235	AAY61927	AAY62132	AAY63263	AAR51652	AAR08270	AAR78749	AAY69213	AAVECOSE	20003
	DB	4.	М	~	, rc	m	m	m	m	m	'n	۰ ر	۱ ۵	10	, с	<b>1</b> C	4 (	<b>v</b> (	ካሰ	ا (،	m	m	~	7	0	m	~	ו
	Query Match Length	9	9	G	9	9	9	9	9	٥		4	. 4	. 4	٠ ٦	יט יי	7 4	0 (	۰ ۵	ים	•	9	4	ιΩ	2	. 2	ľ	ז
o <del>k</del> e	Query	100.0	68.4	65.8	65.8	65.8	63.2	60.5	60.5	60.5	60.5	57.9		57.9			•				വ	s)	N	-	•	52.6	52.6	
	Score	38	26	25	25	25	24	23	23	23	23	22	22	22	22	22	20	100	10	1 6	77.	17	20	20	20	20	20	
	Result No.	П	7	e	4	2	9	7	∞	σι	10	11	12		14	15	16	17	18	0 0	9 6	0.0	21	22	23	24	25	

Aay68185 Haemoglob Aag78351 Haemoglob Abb83467 Tissue Ta		ADD//196 Haemoglob ADD/7197 Haemoglob	Aaw08703 Honeybee				Aay09380 Immunoact	Adwestis fumour ne Aabsans Aic			Abb46600 Desmocoll		Aaw43270 Peptide # Aay29743 Artificia
		5 5 ABB77197		7	0,0		1 (2)	m	m	4,1	6 5 ABB46600	0.0	5 2 AAY29743
000	20 52.6 20 52.6	20 52.6			20 52.6	25.	20 52.6	52.	52.	30 52.6	525	9 50.	19 50.0
22.0	308	31	3 6	€. t	ያ የ	37	38	98.	4 ¢	1.4	43	44	45

# ALIGNMENTS

AAU04531 standard; peptide; 6 AA. VEGF based monocyclic peptide 9. (first entry) 26-SEP-2001 AAU04531; RESULT 1
AAU04531
ID AAU04531
XX
AXC AAU0.
XX
DT 26-S
DE VEGF
XX
CO VEGF
XX
CO VEGF
CC VEGF
CC

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

1. .6 /note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond

WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Hughes RA,

Achen MG,

Stacker S,

Cendron A;

WPI; 2001-442248/47

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

WPI; 2000-038791/03.

```
peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

CC for cyclisation are used to interfere with angiogenesis.

CC nevascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC The condition is diabetic retinopathy, psoriasis, arthropathy.

CC The condition is diabetic retinopathy, psoriasis, arthropathy.

CC The condition is diabetic retinopathy, psoriasis, arthropathy.

CC trauma, substance-induced neovascularisation of the liver, excessive creature, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, nor chronic liver confection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inacaterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inacaterised by that least one biological activity induced by VEGF, VEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chipper contonic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-11; cadherin-18; T-cadherin; PB-cadherin; protocadherin; cadherin related neuronal receptor; II-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 38; DB 4; Length 6; 100.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 1..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY61488 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-00234395.
99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00073040.
98US-00187859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-CA000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurological disease; cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY61488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY6148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                   $$$$$$$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
comprising peptides which comprise a nonclassical cadherin cell adhesion comprising peptides which comprise a nonclassical cadherin cell adhesion comprising peptides which comprise a nonclassical cadherin cell adhesion (CRR) sequence. The Mas can be used for e.g. nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, chancing delivery of a drug through the skin of a mammal, command, inhibiting adhesion of a tumour in a mammal, treating cancer in an angious cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cell, preventing or treating obesity in a mammal, stimulating concreasing cell, preventing or treating obesity in a mammal, stimulating concreasing vasopermeability in a mammal, enhancing adhesion of contrant nervous system, treating demyelinating neurological disease, concreasing vasopermeability in a mammal, enhancing adhesion of concreasing vasopermeability in a mammal, enhancing schaltity in nonclassical cadherin-expressing cells, inhibiting synaptic stability in nonclassical cadherin-expressing cells, inhibiting synaptic stability in conclassical cadherin-expressing cells, inhibiting son also be used for treating ed. psortasis, arthritis, age conclained macular degeneration, multiple sclerosis and diabetes. The mammal. They can also be used for treating ed. psortasis, and an anamolation and diagnosis and in bioreactors. Any 60592 to AAN 66432 used for the ed. the processing in the proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-15; T-cadherin; PB-cadherin; cadherin-15; T-cadherin; PB-cadherin; desmocnal receptor; LI-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatcid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                               New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                        The present invention describes cadherin modulating agents (MA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68.4%; Score 26; DB 3; Length 6; 66.7%; Pred. No. 1.46+06; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                   Claim 36; Page 172; 252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY62223 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEPKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MO9957149-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY62223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY62223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
à
```

Location/Qualifiers 1.6

Disulfide-bond

W09957149-A2

11-NOV-1999

Homo sapiens.

Synthetic

(ADHE-) ADHEREX TECHNOLOGIES INC.

98US-00187859. 99US-00234395. 99US-00264516.

20-JAN-1999; 08-MAR-1999; 05-MAY-1998; 06-NOV-1998;

99WO-CA000363 98US-00073040

05-MAY-1999;

```
The present invention describes cadherin modulating agents (MA)

Comprising peptides which comprise a nonclassical cadherin cell adhesion

Comprising peptides which comprise a nonclassical cadherin cell adhesion

Comprising bettides which comprise a nonclassical cadherin cell adhesion

Comprision cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, changenesing delivery of a drug through the skin of a mammal, and ammal, inhibiting metastasis of a cancer in a mammal, inhibiting sample cell, preventing or treating about delivery to the capressing cell, preventing or treating demyelinating neurological disease, increasing vacopermeablilty in a mammal, enhancing adhesion of conclassing vacopermeablilty in a mammal, enhancing adhesion of conclassing vacopermeablilty in a mammal, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age correlated macular degeneration, multiple sclerosis and diabetes. The mammal. They can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The products can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The AAY64572 represent specifically claimed peptides, and companient companient companient sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                          New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                    Claim 54; Page 184; 252pp; English.
                                                                                                                                                          (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY62763 standard; peptide; 6 AA.
                                                                                                                                                                                                            Byers S;
  99WO-CA000363.
                                                                  98US-00187859.
99US-00234395.
                                                                                                             99US-00264516.
                                               98US-00073040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                    Gour BJ,
                                                                                                                                                                                                                                                    WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVPLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6 AA;
                                                                06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                    Blaschuk OW,
  05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

```
.
0
                                                                                                                                                                                                                                                                                                                                              Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-18; cadherin-12; cadherin-15; T-cadherin; PB-cadherin; cadherin-15; T-cadherin; DB-cadherin; protocadherin; desmoglein; desmoglein; desmocollin; calcium binding; cancer; tumour; obesity; rhemmatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                           Gaps
                                                                                                                                                                                                                                                                                                        PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4046.
                                          .;
Score 25; DB 3; Length 6;
Pred. No. 1.4e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                         02-MAR-2000 (first entry)
                                                                                                                                                                                                                                       AAY62763;
```

```
The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion erecognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, channed delivery of a drug through the skin of a mammal, channed delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cacles, preventing or treating obesity in a mammal, stimulating contral nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of conclassical cadherin-expressing cells, inhibiting symptic stability in a mammal. They can also be used for cor reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e dihesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors.

**NEWARDS***

**Comparison***

**Comparison***

**Comparison**

**Compariso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cadherin-12 cell adhesion recognition cyclic peptide SEQ ID NO:1798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.8%; Score 25; DB 3; Length 6; 66.7%; Pred. No. 1.48+06; ive. 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 72; Page 193; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY62006 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CVPLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDPKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY62006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY62006
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BXHXAX
```

OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin; cadherin; cadherin; protocadherin; cadherin; cadherin; protocadherin; cadherin; calcin binding; cancer; tumour; obesity; rhewmatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.

Location/Qualifiers

Disulfide-bond

WO9957149-A2

Homo sapiens

Synthetic.

99WO-CA000363. 98US-00073040. 98US-00187859. 99US-00234395.

05-MAY-1999;

11-NOV-11999

05-MAY-1998; 36-NOV-1998; 20-JAN-1999; 08-MAR-1999; (ADHE-) ADHEREX TECHNOLOGIES INC.

cadherin extracellular domain; cell adhesion recognition;

Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3573. nonclassical cadherin mediated cell adhesion; CAR;

(first entry)

02-MAR-2000

AAY64259;

Modulation; inhibition;

AAY64259 standard; peptide; 6 AA

RESULT 6 AAY64259

```
New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
    Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; cadherin; cadherin-5; cadherin-7; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin-16; cadherin; p-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; resemble colling; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                Claim 48; Page 180; 252pp; English
                                                                                                                                                                                                                                                                                       (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                   98US-00073040.
98US-00187859.
                                                                                                                                                                                                                                                                    99US-00264516.
                                                                                                                                                                                                              99WO-CA000363
                                                                                                                                                                                                                                                        99US-00234395
                                                                                                                                                                                                                                                                                                             Blaschuk OW, Gour BJ,
                                                                                                                                                                                                                                                                                                                                 WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                               Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6 AA;
                                                                                                                                                                      WO9957149-A2
                                                                                                                  Homo sapiens
                                                                                                                                                                                                             05-MAY-1999;
                                                                                                                                                                                                                                    05-MAY-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                    08-MAR-1999;
                                                                                                                                                                                          11-NOV-11999
                                                                                                                                                                                                                                                          20-JAN-1999
                                                                                                        Synthetic
```

Byers S;

```
The present invention describes cadherin modulating agents (MA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

comprising peptides which comprise a nonclassical cadherin cell adhesion

crecognition (CAR) sequence. The MAs can be used for modulating adhesion of nonclassical-cadherin expressing cells in a

inhibiting adhesion of nonclassical-cadherin expressing cells in a

comman, enhancing delivery of a drug through the skin of a mammal,

companies in a mammal, inducing apoptosis in a monclassical cadherin-

expressing cell, preventing or treating obesity in a mammal, stimbiting

compressing cell, preventing or treating obesity in a mammal, stimbiting

contral nervous system, treating a demyelinating neurological disease,

contral nervous system, treating a demyelinating adhesion of conclassing vasopermeability in a mammal, enhancing adhesion of conclassing vasopermeability in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

cor reducing act a lesue, or enhancing adhesion of foreign tissue in a

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

cor reducing scar tissue, or enhancing adhesion of products can also be used for treating e.g. psoriasis, arthritis, age

crelated macular degeneration, multiple sclerosis and diabetes. The

conducts can also be used for detection and diagnosis and in bioreactors.

AMY6653 to AAX64572 represent specifically claimed peptides, and

cor recognition of the prosent invention and diagnosis and in bioreactors.

cor the conducts of the prosent invention and diagnosis and in bioreactors invention and conducts and in processing and in processing end in the processing edges of the processing edges of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.8%; Score 25; DB 3; Length 6; 66.7%; Pred. No. 1.4e+06; 2; Indels ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention
```

ö

Gaps

.; 0

0; Mismatches

4; Conservative

Matches

CVPLTC 6 CDPKTC 6

à d

```
The present invention describes cadherin modulating agents (WA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

recognition (CAR) sequence. The MAs can be used for modulating

nonclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

mammal, enhancing delivery of a drug through the skin of a mammal,

control and inhibiting metastasis of a cancer in a mammal, tinhibiting

angiogenesis in a mammal, inducing apoptosis in a nonclassing call cadherin-

expressing call, preventing or treating obesity in a mammal, stimulating

contral nervous system, treating a demyelinating neurological disease,

contral nervous system, treating a demyelinating neurological disease,

conclassing vasopermeablity in a mammal. Hely can also be used for

conclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for treating e.g. psoriasis arthritis, age

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

cor reducing scar tissue, or enhancing adhesion of diadnosts and in bioreactors.

ANY64572 to AAX64572 represent specifically claimed peptides, and

AAX64573 to AAX64572 represent specifically claimed peptides, and

cor handlessing of he was an and AAX33188 of represent sequences used in

cor handlessing and AAX33183 to AAX33186 represent sequences used in
                                                                                                                                                                                                  New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 102; Page 217; 252pp; English.
Byers S;
Gour BJ,
                                                                                                            WPI; 2000-038791/03
Blaschuk OW,
```

ö

Gaps

.; 0

```
Interleukin-2; IL-2; antiinflammatory; antiarthritic; antirheumatic;
                                                                                                                                             antidiabetic; neuroprotective; dermatological; immunosuppressive; opthalmological; autoimmune disease; multiple sclerosis; uveitis; systemic lupus erythematosus; Crohn's disease.
           Score 24; DB 3; Length 6;
Pred. No. 1.4e+06;
2; Mismatches 1; Indels
                                                                                                                          IL-2 derived anti-inflammatory peptide pep11.
                                                                                   AAY85373 standard; peptide; 6 AA.
            63.2%;
                                                                                                              (first entry)
                          3; Conservative
           Query Match
Best Local Similarity
                                       9
                                                   9
                                      CVPLTC
                                                  CDPVSC
                                                                                                                                                                                           WO200011028-A2.
Sequence 6 AA;
                                                                                                              19-JUN-2000
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                        Synthetic
                                                                                                AAY85373;
                         Matches
```

98GB-00018370. 98IL-00126009. 99IL-00129980. 99WO-IL000448 19-AUG-1999; 21-AUG-1998; 31-AUG-1998; 16-MAY-1999; 02-MAR-2000.

Yavin EJ, Fridkin M; Ariel A, Hershkoviz R, Lider O,

(YEDA ) YEDA RES & DEV CO LID.

WPI; 2000-256367/22.

Synthetic antiinflammatory peptide derived from IL-2 and its derivatives useful for treating inflammatory autoimmune diseases such as rheumatoid arthritis, multiple sclerosis and systemic lupus erythematosus.

Claim 6; Page 35; 49pp; English.

The invention provides synthetic antiinflammatory peptides derived from interleukin-2 (IL-2). They can be used for inhibition of adhesion of activated T-cells to ECM proteins such as fibronectin, laminin, collagen type-IV; inhibition of Chemotactic migration of T-cell through BCM proteins preferably fibronectin; inhibition of syntheme or mitogen induced T-cell proliferation; inhibition of spontaneous or induced, preferably TNF-1lpha induced cytokine secretion (e.g.IL-8, IL-1beta) by stimulated T-cells and intestinal peithelial cells. The anti-inflammatory peptides and their derivatives are useful for preparing compositions for treating and/or alleviating chronic or acute inflammatory disorders and autoimmune diseases such as rheumatoid arrhitis, diabetes type-I, multiple sclerosis, systemic lupus erythematosus, bowel inflammation, uveitis, and Crohn's disease. Sequences AAY85366-374 represent modified anti-inflammatory derivative peptides derived from the IL-2 derived anti-inflammatory peptide pept (AAY85363)

Sequence 6 AA;

```
ö
                            Gaps
                            .;
0
  Score 23; DB 3; Length 6;
Pred. No. 1.4e+06;
1; Mismatches 2; Indels
 60.5%;
                        Conservative
             Best Local Similarity
Query Match
                       Matches
```

```
Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-15; cadherin-6; cadherin-7; cadherin-18; cadherin-12; cadherin; pB-cadherin; protocadherin; cadherin-16; T-cadherin; pB-cadherin; protocadherin; cadherin; cadherin; cadherin; cadherin; protocadherin; desmoglelin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
expressing cell, preventing or treating obesity in a mammal, stimulating
blood vessel regression in a mammal, enhancing drug delivery to the
central nervous system, treating a demyelinating neurological disease,
increasing vasopermeability in a mammal, enhancing adhesion of
anorlassical cadherin-expressing cells, inhibiting synaptic stability in
a mammal, or preventing pregnancy in a mammal. They can also be used for
e.g. enhancing or directing neurite outgrowth, facilitating wound healing
or reducing scar tissue, or enhancing adhesion of foreign tissue in a
mammal. They can also be used for treating e.g. psoriasis, arthritis, age
related macular degeneration, multiple sclerosis and diabetes. The
products can also be used for detection and diagnosis and in bioreactors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
                                                                                                                                                                                                                                                        PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 72; Page 193; 252pp; English
                                                                                                                                     AAY62757 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00234395.
99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00073040.
98US-00187859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-CA000363
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-038791/03.
  9
                                     φ
  CVPLTC
                      |: | |
1 CIVLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blaschuk OW,
                                                                                                                                                                                                                    02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAY-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1999
Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                             AAY62757;
                                                                                                                  AAY62757
                                                                                                RESULT
                                                                                                                                                                           q
à
```

```
AAY44431
                                                                                                                                                                                                                                                                                                                                     2222222222222222
                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                         ò
                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                               Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; cadherin; cadherin-6; cadherin-6; cadherin-12; cadherin-15; cadherin-15; cadherin; pB-cadherin; cadherin-15; T-cadherin; pB-cadherin; cadherin-15; T-cadherin; protocadherin; cadherin; cadherin; cadherin; desmocollin; desmocollin; desmocollin; calcium binding; cancer; tumour; obesity; rhemmatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The Mas can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug to through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, reating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating
            'n
AAY60592 to AAY64572 represent specifically claimed peptides, and AAY64573 to AAY64643 and AAZ331B3 to AAZ331B6 represent sequences used the exemplification of the present invention
                                                                                               Gaps
                                                                                                                                                                                                                                                                           cell adhesion recognition cyclic peptide SEQ ID NO:2154.
                                                                                               ..
0
                                                                      Score 23; DB 3; Length 6;
Pred. No. 1.4e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 60; Page 188; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                         AAY62488 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00073040.
98US-00187859.
99US-00234395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-CA000363.
                                                                                                                                                                                                                                                      02-MAR-2000 (first entry)
                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-038791/03.
                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                       CDELTC 6
                                                                                                                       1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                 Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-1998;
                                                                                                                                                                                                                                                                              Cadherin-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-NOV-11999
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                           8\%
                                                                                                                        ò
                                                                                                                                              셤
```

```
The present sequence is a peptide fragment derived from domain 1 of human beta-2 glycoprotein, a phospholipid binding serum protein. Isolated domain 1 of beta-2 GPI protein binds to and inhibits beta-2 GPI dependent antiphospholipid antibodies. The fragments are useful as toleragens when they bind to the antibodies at the surface of a B cell and triggers when they bind to the antibodies and mimetics can be used for treating discorders associated with beta 2GPI-dependent aPI-associated pathologies, of thrombosis, recurrent feetal loss, thrombocytopenia or autoinmune diseases such as systemic lupus erythematosus. The polypeptides can also be used to detect and purify antibodies. They can also be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAV60592 to AAV64572 represent specifically claimed peptides, and AAV64573 to AAV64433183 to AAZ3186 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated domain 1 beta-2 GPI polypeptides, used for inhibiting antiphospholipid antibodies for treating, e.g. thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toleragen; B cell anergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide 1 derived from domain 1 of human beta-2 glycoprotein I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta-2 glycoprotein I; beta-2 GPI; toleragen; B cell ar beta-2 GPI-dependent antiphospholipid antibody; thrombosis; recurrent foetal loss; thrombocytopenia; autoimmune disease; systemic lupus erythematosus; coagulation assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linnik MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.5%; Score 23; DB 3; Length 6; llarity 66.7%; Pred. No. 1.4e+06; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marquis DM, Iverson GM, Victoria EJ, Jones DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 19; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44431 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0088656P.
98US-0103088P.
99US-00328199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US013194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LJOL-) LA JOLLA PHARM CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-116542/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVPLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDELIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUN-1998;
05-OCT-1998;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9964595-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
```

SXC

à

```
Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include a family of tetrapeptides based on the recognition site (AAR49776) of farnesyltransferase (FT), are potential anticancer agents that inhibit FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New farnesyl-transferase inhibitors - used for inhibiting attachment of farnesyl molety to a p21ras protein in malignant cells.
                                                                                                                                                 Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22; DB 2; Length 4;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Farnesyl transferase inhibitor tetrapeptide, CVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Farnesyl transferase; inhibitor; cancer; ras; p21
                                                                                                                                                                                                                                                                                                                                                                                                              Marsters JC;
                                                                                                                                                                 ras protein; farnesylation; cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Page 33; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Reiss Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR77833 standard; protein; 4 AA.
   AAR49769 standard; peptide; 4 AA.
                                                                                                                 Farnesyltransferase-inhibitor.
                                                                                                                                                                                                                                                                                                                              92US-00935087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 57.9%;
Similarity 75.0%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                           (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                            Goldstein JL,
                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-083105/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4 AA;
                                                                                                                                                                                                                              WO9404561-A1
                                                                                                                                                                                                                                                                                              24-AUG-1993;
                                                                                                                                                                                                                                                                                                                             24-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
23-JAN-1996
                                                                25-MAR-2003
08-AUG-1994
                                                                                                                                                                                                                                                                03-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5420245-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1995
                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                            Brown MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR77833;
                                 AAR49769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR77833
   ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This peptide or the peptides represented in AAR15751-81, AAR14723 and AAR14711 inhibit the rat FTs represented in AAR14712-22. They show FT inhibition at an ICSO of 0.01-10 microM. The most potent inhibitors are ones in which phenylalanine occurs at the third position of a tetrapeptide whose N-terminus is cysteine. The inhibitors have a farnesyl acceptor or inhibitor sequence within its structure and are capable of inhibiting the farnesylation of palras by FT. See also AAR14711-23 and AAQ14541-47. (Updated on 09-AAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compsn. comprising purified farnesyl-protein transferase - used to inhibit attachment of farnesyl moiety to RAS protein in malignant cells and to treat cancer.
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                             60.5%; Score 23; DB 3; Length 6; 50.0%; Pred. No. 1.4e+06; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 75.0%; Pred. No. 1.4e+06; Similarity 75.0%; Pred. No. 1.4e+06; Similarity 75.0%; Pred. No. 1.4e+06; Similarity 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Farnesyl; transferase; FT; inhibitor; p21ras; rat.
                                                                                                                                                                                                                                                                                                                                                                          Farnesyl-protein transferase inhibitor (25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goldstein JL, Reiss Y;
                                                                                                                                                                                                                                           AAR15772 standard; protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Page 68; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90US-00510706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-00510706
90US-00615715
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TEXA ) UNIV TEXAS SYSTEM.
                                                              Query Match 60.5
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                             (revised)
                                                                                                                                                                                                                                                                                                                             revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-339750/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
coagulation assays
                                                                                                                               1 CVPLTC 6
                                                                                                                                                               9
                                                                                                                                                             CTPRVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVPL 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVPM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4 AA;
                                Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L8-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1990;
                                                                                                                                                                                                                                                                                                            25-MAR-2003
                                                                                                                                                                                                                                                                                                                         09-JAN-2003
29-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9116340-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brown MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                           AAR15772;
```

RESULT 11
AAR15772
IAAR15772
XX
AAR15772
XX
AAR15
DT 25-MI
DT 29-JJ
DT 29-J

ö

Gaps

·,

92US-00863169 90US-00510706

03-APR-1992; 18-APR-1990;

RESULT 12 AAR49769

Matches

ð

Ø

```
Hepatitis C virus
                                                                                                                                             1 CVPL 4
                                                                                                                                                                   CVPM 4
                                                              K-RasB protein
                                                                                  Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP10226698-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-FEB-1997;
                                                                                                                                                                                                                                                             02-MAR-1999
                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                         AAW67428;
                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                            AAW67428
 88888888
                                                                                                                                                                 g
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                               transferase. They all obey a generic formula for the C-terminal sequence of 4-10 amino acid inhibitory peptides; the formula is -CAAX, where C= cysteane, A= any alighatic, aromatic or hydroxy amino acid and X= any normal amino acid. Farnesyl transferase is involved in the farnesylation of various cellular proteins including the cancer related ras proteins. The transforming activity of ras is dependent on the localisation of the protein to membranes, a property which is thought to be dependent upon treating cancers and rask-groups. The peptide inhibitors are useful for treating cancers and rask-rabated cancers in particular. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                      acceptor substrate carboxy terminal sequences, used for the treatment of
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assay for farnesyl transferase activity - by determining ability to transfer farnesyl moiety to K-Ras B protein, partic. useful for identifying inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farnesyl transferase, inhibitor, cancer; tumour, neoplasia, prenyl; ras protein, K-ras B; malignant, detection; identification.
                                                                                           New farnesyl transferase inhibitor peptide(s) - based on farnesyl
                                                                                                                                                       AAR77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farnesyl transferase peptide inhibitor used in cancer treatment.
                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                         Score 22; DB 2; Lengtn 4,
Pred, No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 34; 257pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            James GL;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04459 standard; peptide; 4 AA.
                                                                                                                                    Claim 2; Col 62; 55pp; English.
                                                                                                                                                                                                                                                                                                   57.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US005969.
90US-00615715
92US-00822011
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                          3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown MS, Goldstein JL,
                                                   Goldstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-497642/49.
                                                                       WPI; 1995-206308/27
                              (TEXA ) UNIV TEXAS
                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                          |||:
CVPM 4
                                                                                                                                                                                                                                                                                                                                              1 CVPL 4
                                                                                                                                                                                                                                                                                  Sequence 4 AA;
20-NOV-1990;
16-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9634113-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW04459
                                                                                                                                                                                                                                                                                                     Query Match
                                                   Reiss Y,
                                                                                                                 cancer.
                                                                                                                                                                                                                                                                                                                         Matches
 ઠે
                                                                                                                                                                                                                                                                                                                                                                 d
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an analogue peptide of the Hepatitis C virus HCV) mucleocappid core protein. The invention relates to peptide analogues derived from HCV proteins, e.g. AAMG7417-WG7426, which can be used for the determination of anti-HCV antibodies in a sample. Preferably the peptide analogues contain one or more thloanide peptide bonds where at least one oxygen atom of the peptide bond is replaced by sulphur atom. The peptide analogues can be adsorbed or chemically bound to a carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus, HCV; nucleocapsid, core protein; analogue, antibody; non-structural protein; thioamide bond, peptide bond.
AAW04433-W04465 are peptide inhibitors of farnesyl transferase (FT) activity. The peptides block the attachment of prenyl groups to ras proteins in malignant cells of patients suffering from cancer or a precancerous state and as such are used to treat cancer. The peptides were identified by determining the ability of candidate substances to inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ör
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ပ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determination of antibody in sample - uses peptide analog absorbed chemically bound on carrier as antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "side chain protected by benzoyl group and terminus protected by benzyl group"
                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "side chain protected by butyl group"
                                                                                                                                                                                                                                                                                                             Score 22; DB 2; Length 4;
Pred. No. 1.4e+06;
L; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "side chain protected by tosyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 22; DB 2; I
Pred. No. 1:4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 9; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW67428 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                             57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97JP-00034702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-00034702
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV peptide analogue #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ř.
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-515103/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KYOW ) KYOWA MEDEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
```

1; Indels 4; Conservative 0; Mismatches Matches

0;

0; Gaps

1 CVPLT 5 | | | | 1 CRPLT 5

Sy do

Search completed: September 5, 2004, 11:25:15 Job time : 64 secs

This Page Blank (uspto)

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                      September 5, 2004, 11:26:47; Search time 67 Seconds (without alignments) 28.215 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1298764 segs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                             US-09-761-636A-12
38
1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 6
                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                             Run on:
```

		Appl	1374, Ap	1374, Ap	1798, Ap	3970, Ap	4046, Ap	1798, Ap	3970, Ap	4046, Ap	75, Appl	3573, Ap	3573, Ap	2154, Ap	4040, Ap	2154, Ap
	по	12	). (e	e 1									e 3	e 2		
	Description	Sequence 12, App]	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence						
)		US-09-761-636A-12	US-10-006-869-1374	JS-10-395-032-1374	JS-10-006-869-1798	US-10-006-869-3970	US-10-006-869-4046	US-10-395-032-1798	US-10-395-032-3970	US-10-395-032-4046	US-10-422-571-75	US-10-006-869-3573	US-10-395-032-3573	US-10-006-869-2154	JS-10-006-869-4040	JS-10-395-032-2154
	ΠD	US-09-76	US-10-0	US-10-3	US-10-0	US-10-0	US-10-0	US-10-3	US-10-3	US-10-3	US-10-4	US-10-0	US-10-3	US-10-0	US-10-0	US-10-3
	DB	6	14	15	14	14	14	15	15	15	16	14	15	14	14	15
	j Query Match Length DB	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
ď	Query Match	100.0	68.4	68.4	65.8	65.8	65.8	65.8	65.8	65.8	65.8	63.2	63.2	60.5	60.5	60.5
	Score	38	26	26	25	25	25	25	25	25	25	24	24	23	23	23
	Result No.	1	7	Э	4	Ŋ	9	7	α	6	10	11	12	13	14	15

ö

; Sequence 1374, Application US/10006869 ; Publication No. US20030082166A1

RESULT 2 US-10-006-869-1374

Sequence 4040, Ap Sequence 35, Appl Sequence 103, App Sequence 1737, Ap Sequence 2719, Ap		274 274 198 198 274	თთთσ	, e e e e e e e e e e e e e e e e e e e
044000C	US-10-395-032-2719 US-09-911-838-184 US-09-911-838-186 US-09-792-286-222 US-09-792-286-226	-869-18 -869-27 -513-9 -032-18	-753-139 -416-797 911-838- 911-838- 911-838-	- 935-430 - 006-869- - 271-343- - 436-826- - 277-292- - 280-340-
2 4 1 1 1 4 4 1 1 5 1 5 1 5 1 5 1 5 1 5 1	2 6 6 7 6 7	4444 54445	100000	71111111111111111111111111111111111111
040000	<u>, , , , , , , , , , , , , , , , , , , </u>	<i>ဎ ဎ ဎ ဎ ဎ</i> ၓ	<b>2</b>	<i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>
	م ښښښښږ	نسسسس	999999	
57 57 57 57 57	55 55 55 55 55 55		222222	222222222222222222222222222222222222222
# # # # # # # # # # # # # # # # # # #	22112	21 21 21 21 21 21 21 21 21 21 21 21 21 2	000000	000000000000000000000000000000000000000
16 117 118 119 220 220	0 0 0 0 0 0 0 6 4 6 9 6	8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	33 3 3 4 4 3 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	39 9 4 4 4 4 4 4 4 4 4 4 4 4 4 4 5 5 4 4 5 5 4 5 5 4 5 5 6 5 6

# ALIGNMENTS

```
US-09-761-636A-12

Sequence 12, Application US/09761636A
Sequence 12, Application US/09761636A
Sequence 12, Application US/09761636A
Sequence 12, Application US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Ascven
APPLICANT: ATACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/4850S Achen et al
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR PILING DATE: 2000-01-18
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
PRIOR PRIOR PRIOR OF PRIOR OF PRIOR OF PRIOR PRIOR OF PRIOR PRIOR OF PRIOR PRIOR OF PRIOR OF PRIOR OF PRIOR PRIOR OF PRIOR PRIOR OF PRIOR PRIOR OF PRIOR OF PRIOR PR
```

```
SEQ ID NO 4046
LENGTH: 6
TYPE: PRT
                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
           APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADABEAIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.1374
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: GOUR, Barbara J.
TITLE OF INVENTION: COMPOUNS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100066.407C9
CURRENT APPLICATION NUMBER: US/10/395,032
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blaschuk, Orest w. APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Gour, Barbara J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS FILE REFERENCE: 100086.407C7
                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-7 cell adhesion recognition sequence US-10-006-869-1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
CTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-10-395-032-1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.4%; Score 26; DB 14; Length 6; 66.7%; Pred. No. 1.2e+06; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 68.4%; Score 26; DB 15; Length 6; Best Local Similarity 66.7%; Pred. No. 1.2e+06; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 1798, Application US/10006869; Publication No. US20030082166A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1374, Application US/10395032 Publication No. US20030229199A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ČEPKTČ 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CEPKTC 6
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-395-032-1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-869-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Blaschuk, Orest W. APPLICANT: Blaschuk, Orest W. APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Gour, Barbara J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CAMPOINTED FUNCTIONS FILE REFERENCE: 100086.407C7 CURRENT FILING DATE: 2001-12-03 NUMBER OF SEQ ID NOS: 4052 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4046, Application US/10006869
Publication No. US20030082166A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-10-006-869-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-10-006-869-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                         Query Match 65.8%; Score 25; DB 14; Length 6; Best Local Similarity 66.7%; Pred. No. 1.2e+06; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.8%; Score 25; DB 14; Length 6; 66.7%; Pred. No. 1.2e+06; Live 0; Mismatches 2; Indels
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1798
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3970, Application US/10006869; Publication No. US20030082166A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 4; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-10-006-869-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-006-869-3970
```

ö

à g

```
APPLICANT: Jakobovits, Aya
APPLICANT: Jakobovits, Aya
APPLICANT: Faris, Mary
APPLICANT: Ge, Wangmao
TITLE OF INVENTION: Nucleic Acids and Corresponding Proteins
TITLE OF INVENTION: Entitled 191P4D12(b) Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer;
FILE REPERENCE: 5013-04-23
FILE REPERENCE: 5013-04-23
FURBENT APPLICATION NUMBER: US60/404,306
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-11-01
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 75
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                         Sequence 4046, Application US/10395032

Sequence 4046, Application US/10395032

Publication No. US20030229199A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TILLE REFERENCE: 100086 407C9

CURRENT APPLICATION NUMBER: US/10/395,032

CURRENT FILING DATE: 203-03-21

NUMBER OF SEC ID NOS: 4052

SOFTWARE: Patentin Ver. 2.0

SEC ID NO 4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-10-395-032-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·:
                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
   Pred. No. 1.2e+06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.8%; Score 25; DB 16; L 100.0%; Pred. No. 1.2e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.8%; Score 25; DB 15;
66.7%; Pred. No. 1.2e+06;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-422-571-75; Application US/10422571; Sequence 75, Application US. US20040083497A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raitano, Arthur B.
Challita-Eid, Pia M.
Jakobovits, Aya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 4; Conservative
                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Agensys, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
      Best Local Similarity
                                                                                                    1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CDPKTC 6
                                                                                                                                                             1 CDPKTC
                                                                                                                                                                                                                                                          RESULT 9
US-10-395-032-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-422-571-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                    ਨੇ
                                                                                                                                                                윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1798, Application US/10395032
Fublication No. US20030229199A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour. Barbara J.
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C99
CURRENT APPLICATION WHERE: 2003-03-21
CURRENT APPLICATION WHERE: 2003-03-21
CURRENT PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-395-032-3970

Sequence 3970, Application US/10395032

Publication No. US20030229199A1

Sequence 3970, Application US/10395032

Publication No. US20030229199A1

Sequence 3970, Application No. Sequence No. Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                 Gaps
                                                            OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-10-006-869-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                 ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 15; Length 6; Pred. No. 1.2e+06; 0; Mismatches 2; Indels
                                                                                                                                                                                           Score 25; DB 14; Length 6; Pred. No. 1.2e+06; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15; Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.8%; Score 25;
                                                                                                                                                                                           65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                          1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                      CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-395-032-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-395-032-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

FEATURE:

d

ö

```
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blaschuk, Orest W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.5
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
US-10-006-869-4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-395-032-2154
                   US-10-006-869-2154
                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                           Sequence 3573, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; FILE REPERRNCE: 100066.40707
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT PILING DATE: 2001-12-03
; SOFTWARE: PATENTIN VET. 2.0
; SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-10-395-032-3573
US-10-395-032-3573
WS-10-395-032-3573
Fublication No. US2003022199A1
GENERAL INFORMATION:
APPLICANT: Blacknuk, Orest W.
APPLICANT: Blacknuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C9
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO 3573
LENGTH: 6
LENGTH: 6
LENGTH: 6
LENGTH: 6
LENGTH: 6
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.2%; Score 24; DB 15; Length 6; 50.0%; Pred. No. 1.2e+06; 2: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24; DB 14;
Pred. No. 1.2e+06;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |::|
1 CDPVSC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |::|
1 CDPVSC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTC 6
PLTC 6
                                       PLTC 6
                                                                                                     RESULT 11
US-10-006-869-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-006-869-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-395-032-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
ò
                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Sequence 2154, Application US/10006869
Publication No. US20030082166A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION UNDMER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: Representative cyclic modulating agent based on corner INFORMATION: cadherin-15 cell adhesion recognition sequence US-10-006-869-2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-10-006-869-4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.5%; Score 23; DB 14; Length 6; 66.7%; Pred. No. 1.2e+06; 2; Indels cive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.5%; Score 23; DB 14; Length 6; 66.7%; Pred. No. 1.2e+06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2154, Application US/10395032; Publication No. US20030229199A1; GENERAL INFORMATION:
```

ö

. 0

```
## APPLICANT: Symonds, James Matthew
### APPLICANT: Symonds, James Matthew
### TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
### TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
### FILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
### CURRENT APPLICATION NUMBER: US/10/395,032
### CURRENT FILING DATE: 2003-03-21
### MWHBER OF SEQ ID NOS: 4052
### SOFTWARE: Patentin Ver. 2.0
### SEQ ID NO 2154
### IENGTH: 6
### TYPE: PRT
### OTHER INFORMATION: Representative cyclic modulating agent based on
### COTHER INFORMATION: Cadherin-15 cell adhesion recognition sequence
### OTHER INFORMATION: Cadherin-15 cell adhesion recognition
### OTHER INFORMATION: Cadherin-15 cell adhesion recognition
### OTHER INFORMATION: Cadherin-15 cell adhesion recognition
### OTHER INFORMATION: CADHERIN CADHER
```

Search completed: September 5, 2004, 11:32:10 Job time : 68 secs

This Page Blank (uspto)

```
1374, Ap
11374, Ap
11374, Ap
3970, Ap
3970, Ap
3970, Ap
3973, Ap
3973, Ap
3973, Ap
2154, Ap
4040, Ap
4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4046, Requence 1798, Requence 3970, Sequence 3573, Requence 3573, Requence 254, Requence 2154, Requenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            2; Search time 20 Seconds (without alignments) 15.488 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1374,
Sequence 1374,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3970,
Sequence 4046,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1798,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgm2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-187-859-1374
US-09-839-542B-1374
US-09-187-859-1798
US-09-187-859-1798
US-09-187-859-3970
US-09-839-542B-1798
US-09-839-542B-1798
US-09-839-542B-4046
US-09-187-859-3573
US-09-187-859-3573
US-09-187-859-464
US-09-187-859-464
US-09-839-542B-4040
US-09-839-542B-4040
US-09-839-542B-4040
US-09-839-542B-41197
US-09-187-859-1737
US-09-187-859-1737
US-09-187-859-1737
US-09-187-859-1885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                               5, 2004, 11:25:22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents AA:*
                                                                                                                                                                                                                                                                                US-09-761-636A-12
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                        1 CVPLTC 6
                                                                                                                                                                     September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0 Maximum DB seq length: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12648
                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                ritle:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.
```

120, App 120, App 4, Appli 6, Appli 13, Appl 21, Appl 1591, Ap 11670, Ap 10670, Ap 109, App 109, App 101, Appli 101, Appli 101, Appli 101, Appli 20, Appli 20, Appli 20, Appli 21, Appli 22, Appli 23, Appli 24, Appli 26, Appli 27, Appli 28, Appli 28, Appli 29, Appli 20, Appli 20, Appli 20, Appli 20, Appli 20, Appli 20, Appli		Cal	oo	Gaps 0;	ICAL
Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq		FOR MODULATING NONCLASSICAL TIONS	based equence	gth 6; Indels 0;	FOR MODULATING NONCLASSICAL
US-08-548-540-120 PCT-US96-09809-120 US-09-322-791-4 US-09-322-791-6 US-09-394-630-13 US-08-750-142B-21 US-09-187-859-1591 US-09-839-542B-1591 US-09-535-852-1340 US-09-535-852-1670 US-09-535-852-1670 US-09-535-852-1670 US-09-248-588-109 US-08-222-048-181 US-08-222-048-181 US-08-222-048-181 US-08-433-318A-181 US-08-460-384-20 US-09-460-384-20 US-09-460-384-20	ALIGNMENTS	ODS FUNC 8592	e ative cyclic modulating agent 7 cell adhesion recognition s	Score 26; DB 4; Len Pred. No. 3e+05; 0; Mismatches 2;	ZB THODS ED FUN 9,542B
445600000000000000000000000000000000000		ULT 1  09-187-859-1374  equence 1374, Application US/09187859A  atent No. 6358920  ENERAL INFORMATION: APPLICANT: Blaschuk, Orest W. APPLICANT: Gour, Barbara J.  TITLE OF INVENTION: COMPOUNDS AND METH  TITLE OF INVENTION: CADHERIN-MEDIATED  CURRENT APPLICATION NUMBER: US/09/187, CURRENT FILING DATE: 1998-11-06  SOFTWARE: PATENT Ver. 2.0  ERO ID NO. 1374  FENDER OF SEQ ID NOS: 4052	ll Sequence Representative cadherin-7 cel	68.4%; 66.7%; vative	US-0919-542B-1374  US-0919-542B-1374  Sequence 1374, Application US/09839542B  Patent No. 656996  GERRAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: TITLE OF INVENTION: COMPOUNDS AND METHOMER OF INVENTION: COMPOUNDS AND METHOMER PERERENCE: 100086 407D1  CURRENT APPLICATION UNDER: US/09/839, 19  CURRENT APPLICATION UNDER: US/09/839, 19  CURRENT FILING DATE: 2001-04-20  NUMBER OF SEQ ID NOS: 4052  SEQ ID NO 1374  LENGTH: 6  TYPE: PRT
000000000000000000000000000000000000000		7-859-1374 ice 1374, Applice No. 6358920 LINFORMATION: CANT: Blaschuk, CANT: Gour, Bark CANT: GOINVENTION: OF INVENTION: OF INVENTION: NT FILING DATE: NT FILING DATE: NO. 1374 INO. 1374	i: o PRT SM: Artificial E: INFORMATION: Re INFORMATION: ca	Similarity 4; Conserva CVPLTC 6	1374 , Applic 69936 MATION: MATION: Symonds, Symonds, Gour, Ba ENTION: CE: 1000 ICATION: Q ID NOS tentin V
		SULT 1  -09-187-859-1374  Sequence 1374, Applicati Patent No. 6358920  GENERAL INRORMATION: APPLICANT: Blaschuk, Or APPLICANT: Gour, Barbar TITLE OF INVENTION: COM TITLE OF INVENTION: CAD FILE REFERENCE: 100086. CURRENT APPLICATION NUM CURRENT FILING DATE: 19 NUMBER OF SEQ ID NOS: 4 SOFTWARE: PatentIN Ver. LENGTH.	RT M: : : NFC NFC	atch	ULT 2  09-839-542B-1374  equence 1374, Applidatent No. 656996  atent No. 656996  atent No. 656996  atent No. 656996  APPLICANT: Blaschuk  APPLICANT: Symonds  APPLICANT: Gour, B  TITLE OF INVENTION:  TITLE OF INVENTION:  TITLE REFERENCE: 100  CURRENT APPLICATION  CURRENT FILING DATE  NUMBER OF SEQ ID NO.  CURRENT FILING DATE  EQUINO 1374  LENGTH: 6  TYPE: PRT
2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 US-09-187-6 ; Sequence ; Patent NG ; GENERAL 1 ; APPLICAN ; TITLE OF ; TIMBER CURRENT ; NUMBER C ; SOFTWARE ; SEQ ID NG ; TEND NG ; SEQ ID NG	TYPE: TYPE: CORGAN COTHER COTHER COTHER COTHER COTHER	Query Ma Best Loc Matches Qy	RESULT US-09-8 ; Seque ; Seque ; Paten ; GRUER APPL ; TITL
		····			

```
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
FILE REPERRNCE: 100066.4070.
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 405-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.8%; Score 25; DB 4; Length 6; 66.7%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.8%; Score 25; DB 4; Length 6; 66.7%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                        US-09-187-859-4046
; Sequence 4046, Application US/09187859A
; Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CVPLTC 6
                         CVPLTC 6
                                                                  CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-09-839-542B-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-09-839-542B-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-187-859-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4046
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1798, Application US/09187859A

Patent No. 6358920

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 1000086.407C11
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORNATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENT IN VET. 2.0
                                           CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-7 cell adhesion recognition sequence US-09-839-542B-1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Representative cyclic modulating agent based on CHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-09-187-859-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.8%; Score 25; DB 4; Length 6; 66.7%; Pred. No. 3e+05;
                                                                                                                                     Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
                                                                                                                                68.4%; Score 26; DB 4;
66.7%; Pred. No. 3e+05;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.8%; Score 25; DB 4; 66.7%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3970, Application US/09187859A Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                              Query Match
Best Local Similarity 66...
Page 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                        1 CVPLTC 6
                                                                                                                                                                                                                                                               1 CEPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                         US-09-187-859-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-09-187-859-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-187-859-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठे
```

·.

Gaps

; 0

```
Sequence 1798, Application US/09839542B

Fatent No. 656996

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 1000086, 407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-09-839-542B-1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
```

0

. 0

```
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                         CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.2%;
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                 FILE REFERENCE: 100086.407C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |::|
CDPVSC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |::|
1 CDPVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-839-542B-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATI
US-09-839-542B-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-187-859-2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-187-859-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT
                                                                                                                                                                                                                                                                                      LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
; Sequence 3970, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
; APPLICANT: Blaschik, Orest W.
; APPLICANT: Blaschik, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS AND METHOD FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: COMPOUNDS
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3970
; FANCH: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4046, Application US/09839542B
| Patent No. 656996|
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. |
| APPLICANT: Symonds, James Matthew |
| APPLICANT: Symonds, James Matthew |
| APPLICANT: Symonds, James Matthew |
| APPLICANT: Gour, Barbara J. |
| TITLE OF INVENTION: CADMERIN-MEDIATED FUNCTIONS |
| TITLE OF INVENTION UNMBER: US/09/839,542B |
| CURRENT FILING DATE: 2001-04-20 |
| SOFTWARE: PATENTION OF: 2.0 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3573, Application US/09187859A
Patent No. 6538920
GRERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-09-839-542B-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-09-839-542B-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.8%; Score 25; DB 4; Length 6; 66.7%; Pred. No. 3e+05; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 4; Length 6; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CDPKTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-09-839-542B-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-187-859-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
Sequence 3573, Application US/09839542B

Sequence 3573, Application US/09839542B

Patent No. 656996

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILLS REPERENCE: 100086.407D1

CURRENT APPLICATION NUMBER: US/09/839,542B

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3573

LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2154, Application US/09187859A

Patent No. 6358920

Patent No. 6358920

SERENAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Blaschuk, Orest W.

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CABHERIN-MEDIATED FUNCTIONS

FILE REPERENCE: 100086.4070T.

CURRENT APPLICATION NUMBER: US/09/187,859A

CURRENT PILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                    .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                 1; Indels
                                                                                                                                                     63.2%; Score 24; DB 4; Length 6; 50.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB 4; Length 6; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2154
```

0

```
Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                     1 CVPLTC 6
                                                                                                                             1 CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: HOUSTON STATE: TEXAS
                                                                                                                                                                                      RESULT 14
US-09-839-542B-4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4040
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-429-964-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                         qq
                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2154, Application US/09839542B

Patent No. 656996
GENERAL INFORMATION:
PAPPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADABER: WS/09/839, 542B
CURRENT APPLICATION NUMBER: US/09/839, 542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN VET. 2.0
                                                                             OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-09-187-859-4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-15 cell adhesion recognition sequence US-09-839-542B-2154
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                 Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 23; DB 4; Length 6;
Pred. No. 3e+05;
0; Mismatches 2; Indels
                                                                                                                                                               60.5%; Score 23; DB 4;
66.7%; Pred. No. 3e+05;
                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-187-859-4040
; Sequence 4040, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.5%;
                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                           Query Match
Best Local Similarity 66.7*
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                          1 CVPLTC 6
                                                                                                                                                                                                                                                                                1 CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-839-542B-2154
                                                                                                        ; OTHER INFORMATION OF 187-859-2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 4040
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2154
  LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT
                                                          FEATURE:
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                              쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                | Sequence 4040, Application US/09839542B |
| Patent No. 656996 |
| Patent No. 656996 |
| Patent No. 656996 |
| APPLICANT: Blaschuk, Orest W. APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Gour, Barbara J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-09-839-542B-4040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BROWN, MICHAEL S.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: GOLDSTEIN, JOSEPH L.
APPLICANT: GALES, YUVAL
APPLICANT: JAMES, GUT L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·,
                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6;
60.5%; Score 23; DB 4; Length
66.7%; Pred. No. 3e+05;
ive 0; Mismatches 2; Inde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLILING DATE: US/08/429,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.5%; Score 23; DB 4;
66.7%; Pred. No. 3e+05;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UNITED STATES OF AMERICA ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 41, Application US/08429964 Patent No. 5962243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
```

```
CLASSIFICATION: 435
APPLICATION NUMBER: US 07/822,011
FILING DATE: ABANDONED
CLASSIFICATION NUMBER: PCT/US/91/02650
FILING DATE: 18 APR-1991
CLASSIFICATION NUMBER: US 07/615,715
FILING DATE: 10 APPL-1991
CLASSIFICATION NUMBER: US 07/615,715
FILING DATE: 10 APPL-1990
CLASSIFICATION NUMBER: US 07/510,706
FILING DATE: 18 APR-1990 (ABANDONED)
CLASSIFICATION NUMBER: US 07/510,706
FILING DATE: 18 APR-1990 (ABANDONED)
CLASSIFICATION NUMBER: US 07/510,706
FILING DATE: 18 APR-1990 (ABANDONED)
CLASSIFICATION NUMBER: US 07/510,706
FILING DATE: 18 APR-1990 (ABANDONED)
CLASSIFICATION NUMBER: US 02/165
FEDERAL OF DECKET NUMBER: UTSD: 435
FEDERAL OF DECKET NUMBER: UTSD: 416-300
FELEFARM (713) 789-2679
FELEFARM (713) 789-2679
FELEFARM (713) 789-2679
FELEFARM: 79-0924
FELEFA
```

Search completed: September 5, 2004, 11:30:16 Job time: 21 secs

1 CVPM 4

This Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

- protein search, using sw model OM protein

September 5, 2004, 11:31:03; Search time 23 Seconds (without alignments) 41.822 Million cell updates/sec Run on:

US-09-761-636A-13 56 1 CISVPLSVPC 10 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283366 seqs, 96191526 residues Searched: 1101 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* ..... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	MHC H2-L antiden -	glycogen phosphory	Ig heavy chain Cr	chain	vitellogenin, 190k	T-cell receptor be	metallothionein-A	205K exoantigen -	polygalacturonase	T-cell receptor be	major postsynaptic		cytochrome-c oxida	hypothetical prote	$^{\text{chr}}$	myomodulin - Calif	gene Cftr protein	118K stomach cance	alp	amicyanin - Paraco	sphingomyelinase -	protein P7 - curle	aryl hydrocarbon (	alpha-gliadin 4Ha	alpha-gliadin 6Ha	Na+/K+-exchanging	flagellar protein	conopressin S - co	cytochrome-c oxida
E	165546	A60521	C39111	PT0247	A61622	PH0944	I51049	G33098	S62880	PH0926	A42689	B49712	S43630	E86128	B22565	A28340	157018	0	826508	A24407	C39745	D28027	865715	A61218	6121	A32195	E42364	B28495	S77984
DB	1	71	~	7	7	0	7	7	0	7	7	7	7	7	7	7	2	7	~	7	7	7	7	7	7	7	0	7	7
ength	9	5	10	9	10	10	4	80	10	10	<b>a</b> 0	6	10	10	S	7	8	σ	σ	10	10	10	10	10	10	10	5	9	6
	35.7	33,9	ص	$^{\circ}$	30.4	ö	œ.	œ.	œ,	æ,	ė.	ů.	ė.	26.8	ъ.	25.0	ъ.	S	S	S	S	S	S		ņ,	'n	ω.	23.2	
core	10	19	19	18	17	17	16	16	16	16	15	15	15	15	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13
Result No.		7	e	4	S	9	7	œ	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain CRD	hemagglutinin - in	platelet activatin	Fc mu (IgM) recept	phosphoprotein, bo	dnaA protein - Pse	alpha-1,4-glucan-p	hypothetical colla	tryptophyllin, bas	seed protein ws-5	aggrecan - bovine	Ig H chain V-D-J r	neural cell adhesi	T-cell receptor be	nitrate reductase	enamelin f - bovin
PT0268	S51912	B45482	C39398	S11127	B34835	B26206	A35039	A61081	E61491	842620	PH1602	A39690	PH0932	S68802	S10783
8	7	~	7	7	7	7	4	7	7	7	7	7	7	7	7
σ ;	10	10	10	S	9	9	9	7	7	7	7	7	7	90	<b>6</b> 0
23.2	23.2	23.2	23.2	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4
13	13	13	13	12	12	12	12	12	12	12	12	12	12	12	12
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

```
165546
MHC H2-L antigen - mouse (fragment)
```

Enhancer-like sequences and thei' C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 165546
A;Fithe: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequer A;Reference number: 152778; MUID:86106202; PMID:3510743
A;Reference number: 152778; MUID:86106202; PMID:3510743
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
A;Rocossion: 165546
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-6 <RES>
A;Residues: 1-6 <RES>
A;Residues: 1-10 <RES>
A;Cross-references: GB:MI2483; NID:g199565; PIDN:AAA39663.1; PID:g554234

6 Gaps . 0 0; Indels h Similarity 100.0%; Pred. No. 2.8e+05; 3; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 3; Conserv

8 VPC 10 111 2 VPC 4 g ò

Authornate names: glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
NyAlternate names: glycogen phosphorylase b
C.Species: Liza ramada
C.Species: Liza ramada
C.Date: 17-Apr-1993 #text_change 18-Aug-2003
C.Accession: A60521
R.Bonamusa, L. Baanante, I.V.
R.Bonamusa, L. Baanante, I.V.
Comp. Blochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus A;Reference number: A60521
A;Accession: A60521
A;Accession: A60521
A;Residues: 1-5 <BON'
C;Superfamily: glucan phosphorylase
C;Superfamily: glucan phosphorylase
C;Superfamily: glucan phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 33.9%; Score 19; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels 2 ISVP 5 à

2 ISVP 5

g

0

Gaps

.;

0; Indels

```
ISI049
metallothionein-A - rainbow trout (fragment)
C;Species Oncorthynchus mykiss (rainbow trout)
C;Species: 0. Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) meA;Reference number: 151049; MUD:95324545; PMID:7601121
A;Accession: 151049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <OLS>
A;Residues: BMBL;X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 033098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
205K exoantigen - falciparum falciparum falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Species: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: G33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: complete Freund's adjuvant-immunized lymph node A;Note: the authors translated the codon GAC for residue 9 as Glu C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 30.4%; Score 17; DB 2; Length 10; Best Local Similarity 60.0%; Pred. No. 4.8e+03; Matches 3; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.6%; Score 16; DB 2; Length 8; 60.0%; Pred. No. 2.8e+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 28.6%; Score 16; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-8 <NIC>
                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-10 <GOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CASSP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VPLSV 8
       PLTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: G33098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PC 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                            Rivarner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
Aritle: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil A;Reference number: A39111; MUID:91156684; PMID:2000382
A;Accession: C39111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NyContains: vitellin
Cispecies: Lymantria dispar (gypsy moth)
Cjaces: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
CjAccession: A61622
R;Hiremath, S.; Eshita, S.
R;Hiremath, Mol. Biol. 22, 605-611, 1992
A;Title: Furification and characterization of vitellogenin from the gypsy moth, Lymantri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rivamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0247
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PT0247

Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Spacies: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0247
C;Accession: DT0247
                                            Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 18-Oct_1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                33.9%; Score 19; DB 2; Length 10; llarity 71.4%; Pred. No. 2.2e+03; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.4%; Score 17; DB 2; Length 10; Best Local Similarity 60.0%; Pred. No. 4.8e+03; Matches 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
32.1%; Score 18; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vitellogenin, 190k chain - gypsy moth (fragment)
                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 «VAR»
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-9 < YAM>
A, Experimental source: B lymphocyte
C, Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: A61622
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-10 <HIR>
C,Keywords: egg yolk; hemolymph
                                                                                                                                                                                                                                                                                                                                                                      4 ISSPLVV 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ISVPLSV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |: |
2 SAPIDSP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SVPLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PLSVP 9
                                                                                                                    C, Accession: C39111
RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

0

ö

·.

g

```
cytochrome-c oxidase (EC 1.9.3.1) chain VIC, hepatic - rainbow trout (fragment) C;Species Oncorhynchus mykiss (rainbow trout) C;Species 20.0ct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997 C;Accession: S43630 C;Accession: S43630 B. Eur. J. Biochem. 221, 1111-1116, 1994 A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochron A;Recession: S43624; MUID:94237150; PMID:8181469 A;Accession: S43630 A;Accession: S43630 A;Nolecule type: protein A;Residues: 1-10 <FRE> A;Note: the source is designated as Salmo gairdneri
                                                                                                                                                                                                        ATP-binding protein p46 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Raccession: B49712
R;Nigam, S:K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
J. Biol. Chem. 269, 1744-1749, 1994
A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular chap.
A;Reference number: A49712; MUID:94124514; PMID:8294423
A;Reference protein
A;Reference type: protein
A;Residues: L-9 < AKG>
C;Keywords: ATP; endoplasmic reticulum; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E86128
C;Accession: E86128
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Mature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E86128
hypothetical protein Z5903 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Genome: nuclear
C; Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15; DB 2; Length 10;
Pred. No. 1.1e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.8%; Score 15; DB 2; Length 9; 33.3%; Pred. No. 2.8e+05; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 26.8%;
Similarity 75.0%;
3; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VPLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA A; Residues: 1-10 <STO>
                                                                              Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | |
1 IPXXYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LXVP 5
                            6 TSAB 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: E86128
                                                                            2 LKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     843630
                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0926
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergity A;Reference number: PH0891; MUID:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                        polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C;Species: Aspergillus sp.
C;Dacies: Aspergillus sp.
C;Dacies: Aspergillus sp.
C;Dacies: Sc2880
R;Stratilova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A;Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A;Reference number: S62880; MUID:96196586; PMID:8612742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Species: Rattus norvegicus (Norway rat)
C,Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
C;Accession: A42689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Wu, K.; Huang, Y.; Adler, J.; Black, I.B.
Proc. Natl. Acad. Sci. U.S.N. 89, 3015-3019. 1992
A;Title: On the identity of the major postsynaptic density protein.
A;Reference number: A42689; MUID:92212958; PMID:1313576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: mRNA
A,Residues: 1-10 <GOL>
A,Experimental Source: concanavalin A-activated lymphoblast
A,Note: the authors translated the codon AGA for residue 4 as Thr
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.6%; Score 16; DB 2; Length 10; 60.0%; Pred. No. 7.2e+03; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 2; Length 8;
Pred. No. 2.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.6%; Score 16; DB 2; Lv
100.0%; Pred. No. 7.2e+03;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major postsynaptic density protein - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: protein
A,Residues: 1-10 <STR>
C,Keywords: glycosidase; hydrolase
F;4/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 26.8%;
Similarity 75.0%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <WUA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
||| :
||| :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASRP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A42689
                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S62880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
A42689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                    862880
```

ö

ò 엄

.; 0

à g

```
A;Cross-references: GB:AE005174; NID:g12519314; PIDN:AAG59489.1; GSPDB:GN00145; UWGP:Z55 A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics: A;Gene: Z5903
                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                         R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment) C; Species: Gastroclonium coulteri) C; Species: Gastroclonium coulteri C; Decies: Gastroclonium coulteri C; Decession: B22565
R; Klotz, A.V.; Glazer, A.N.
R; Klotz, A.V.; Glazer, A.N.
A; Title: Characterization of the bilin attachment sites in R-phycoerythrin. A; Reference number: A22565; MUID:85182601; PMID:3886644
A; Molecule type: protein
A; Residues: 1-5 < KLO>
                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                    Query Match
26.8%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
25.0%; Score 14; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                   6 LSVPC 10
                                                                                                                                                                                                                                                                  s Łovyć 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LCVP 4
                                                                                                                                                                                                                                                                                                                                               RESULT 15
B22565
                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
```

Search completed: September 5, 2004, 11:35:13 Job time: 23 secs

Title:

```
bufo regula
bos taurus
stomopneute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovis aries
leptinotars
cydia pomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leucophaea
litoria rub
conus stria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homo sapien
mytilus edu
mytilus edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               herpes simp
locusta mig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P29177 bos taurus
P41488 locusta mig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conus purpu
oncorhynchu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           locusta mig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
pachymedusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           thunnus obe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusarium so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          penaeus mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treponema h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          herpes simp
mytilus edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cydia pomon
periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           5, 2004, 11:29:57; Search time 14 Seconds (without alignments) 37.193 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P16224
P30088
P81088
P81735
P82096
P82096
P82097
P82097
P82157
P82157
P83320
P83320
P83320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P24047
P01018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P80336
P30094
                                                                                                                                                                                                                                                       371
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           141681 segs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGMT_BOVIN
LDEX2_LOCMI
COXH_ONCMY
NS1_MCTU
NS1_MCTU
UPA2_HUMAN
TPFY_PACDA
TREY_LEUYA
E101_LITRU
CONO_CONST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COXO_SHEEP
MNP1_LEPDE
ALL6_CYDPO
FUSS_FUSSO
UPA1_HUMAN
FAR5_PENMO
FAR5_PENMO
FAR5_PENMO
SYYT_BUFRE
RT33_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGT CHICK
COXQ RABIT
UPA8 HUMAN
CIPI MYTED
CIP2 MYTED
VP19 HSV1K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPK3_PERAM
VGLG_HSV2B
DNF1_LOCMI
                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                 US-09-761-636A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query
Match Length DB
                                                                                                                                               56
1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                           SwissProt_42:*
                                                                             September
                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 10
                                                                                                                                               Perfect score:
                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                           Sequence:
                                                                                                                                                                                                                          Searched:
                                                                             Run on:
```

Result 8 

suu mig aca aca gus iien iien ero in in in chu						0	
P43172 ascaris suu P41489 locusta mig P42999 squalus aca P32878 oryctolagus P30089 homo sapien P30093 homo sapien P3261 prunus sero P33426 bothrops in P31351 vipera aspi Q9przl oncorhynchu P80332 oncorhynchu		.1.1.63) (6-0-	Buteleostomi; ora; Bovoidea;	O6-methylguanine-DNA  A by stoichiometrically ition to a cysteine saction: the enzyme is hylguanine) + protein hylguanine) + protein OGT METHYLTRANSFERASE	SIMILARITY). 9;	0; Gaps	
7 7 7 7 7 7 7 7 7 7 7 7 7 7 8 8 8 8 8 8		BOVIN MGMT_BOVIN STANDARD; PRT; 9 AA. P29177; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1995 (Rel. 24, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) methyltansferase (BC 2 methyltansferase (BC 2 methyltansinal NA methyltansferase)	Craniata; Vertebrata; Bute cctyla; Ruminantia; Pecora;	DNA DOSİT POSİT PEAC METAY METAY	EPTOR (BY CRC64;	+05; 2; Indels	. 0
DH0822 2 3D	SIME	9 AA. update) nn update) framse	<pre># (Bovine) # (Bovine) # (Butheria; Craniata; Vertebrat # (Butheria; Cetartiodactyla; Ruminantia; # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos) # (Bos)</pre>	the bovine O the bovine O the O-6 position suicide rea ting 6-0-meth tout 6-0-meth COLI ADA AND	AL. Yltransferase. ALKYL GROUP ACCEPTOR 5171A720476047 CRC64 Score 26; DB 1; Le	. 1.4e+05 ches	PRT; 10 AA. ed) sequence update) annotation update)
ASCSU LOCMI LOCMI LOCMI LEABIT HUMAN PRUMAN PRUMAN VIPAS ONCMY	ALIGNMENT	r; nce uj ation methy	aniata (la)	of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of the grant of th	cansfer (L GROU LA7204"		[; nce u <u>r</u> ntion
FAR9 LIMT3 OXYA OXYT UPA3 UPA3 BPP 6 BPP 7 COXE GS09	Æ	PRT; ed) sequence up annotation iteine methy	a; Cre odact; 08822, P.;	lence (1990) /latecyropins : // (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (cont (con	thyltrar ALKYL 325171A7 Score	Pred.	PRT ed) sequen
пананананан		D; Created) Last sec Last and Last and Last cant	dati rtic =23(	sequally yll yll e. DNA = 1 MENT	W Met	. a %	
00000000000000000000000000000000000000		STANDARD; 1. 24, Creat 1. 24, Last 1. 34, Last -protein-cy;	MGMT.  Bos taurus (Bovine).  Eukaryota; Metazoa; Chordata; Cra Mammalia; Eutheria; Cetartiodacty Bovidae; Bovinae; Bos.  NCBI_TaxID=9913;  (1)  SEQUENCE:  TISSUE-Thymus;  MEDLINE=90174912; PubMed=2308822;  Rydberg B., Hall J., Karran P.;	"Active site amino acid sequence of the bomethyltransferase."; Nucleic Acids Res. 18:17-21(1990)!- FUNCTION: Repair of alkylated guanine transferring the alkyl group at the Orresidue in the enzyme. This is a suici irreversibly inactivated!- CATALYTIC ACTIVITY: DNA (containing 6-[procein]-1-Cysteine = DNA (without 6-S-methyl-L-Cysteine = DNA (without 6-WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDERED. IRROMASS THE ALKYL-ACCEPTOR RESIDERED.	U3/4; McMl; FAKITAL. Transferase; Methyltransferase 1 9 ALKYL GROUP A 9 9 97 MW; 325171A72047604 46.4%; Score 26; DB	42 ativ	STANDARD; 1.32, Creat 1.32, Last 1.41, Last
• • • • • • • • • • • • • • • • • • • •		STAN (Rel. 2 (Rel. 3 (Rel. 3	(Bovine)  Hataca; Hataca; Boutheria; Bovinee; D=9913; MWUS; O174912; Hall J.	"Active site amino a methyltransferaes."; Nucleic Acids Res."; -!- FUNCTION: Repair -!- FUNCTION: Repair residue in the residue in the irreversibly ina -!- CATALYTIC ACTIVI [protein]-L-cyste S-methyl-L-cyste -!- SIMILARITY: WITH MHICH ENCOMPASS InterPro: IPRO01497;	13/4; M 1 1 9 9 AA; 9	Similarity 3; Conserv VPLSVPC 10 : :    IPILTPC 9	STAN (Rel. 3 (Rel. 3
		(A) (A) (A) (A) (A) (A) (A) (A) (A) (A)	(Bc Met Met Suth your has; 749 Ha	sife a sife a sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign of the sign	EUU.	imilari ; Cons vPLSVPC : :	
		LT 1 MGMT BOVIN P29177, 01-DEC-1992 01-DEC-1996 Methylated-D	MGMT.  Bos taurus (Bovi Eukaryota; Metaz Mammalia; Buther Mammalia; Buther Bovidae; Bovinae NCBI_TaxID=9913; [1] SEQUENCE. TISSUE_Thymus; MEDLINE=90174912 Rydberg B., Hall	hyltrane hyltrane leic Aci FUNCTIC transfe residue irreven CATALY [protei S-methy SIMILAN SIMILAN	rib; FS repair; TER SITE TER ENCE	e# 00	LT 2 LDCMI LPK2 LOCMI P41488; 01-NOV-1995 01-NOV-1995 28-FEB-2003
		RESULT 1 ID MGMT BOVIN ID MGMT B AC B29177 DT 01-DEC DT 01-DEC DT 01-OCT DE Methyl	MGMT. Bos tauru Bukaryot Bukaryot Bovidae, NCBI_Taxl SEQUENCE SEQUENCE TISSUE=T	Activ Nuclei Nuclei Nuclei Ci Ci Ci Ci Ci Ci Ci Ci Ci Ci Ci Ci Ci	PROSITE; DNA repai NON TER ACT_SITE NON TER SEQUENCE	Local hes	RESULT 2 LPK2 LOCMI ID LPK2 LOCMI ID LA1488; AC P41488; DT 01-NOV-199 DT 28-FEB-200
иппппппччччч 4 Б Ф Г 88 Ф О Н С К 4 Б		RESULT MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY MGMT BY	EUMEMZ-OHZK:	FÉŽI I HÍ	PAC DNP NON ACT NON SEC	Best Loc Matches	RESULT LPK2_L ID L AC P DT 0 DT 0
		RES TO TO DI DI DI DI	00 00 00 00 00 00 00 00 00 00 00 00 00	##88888888888	ZZFFFS C	20 dd	RES LPR 1D AC DT DT

```
1 MATPLVDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LXVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=H37Rv;
                                                                             COXH ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS1 MYCTU
P81135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS1_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Clipperton Island; TISSUE=Venom;
MEDLINE=99388839; PubMed=10461743;
Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                           "Isolation, identification and synthesis of locustapyrokinin II from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity).
--- Intelminative Belongs to the pyrokinin family.
InterPro: IPR011484; Pyrokinin.
PROSITE; PSOR0139; PYROKININ; 1.
Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
MON PRS.

I PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Molîusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                     Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                       MEDLINE=94094539; PubMed=7903606;
Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
                                                                                                                                                                                                                                                   Locusta migratoria, another member of the FXPRL-amide peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB 1; Length 10;
Pred. No. 8.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 1; Length 8; Pred. No. 1.4e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CFAF4271A9D1B772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 4 D-LEUCINE.
8 AA; 890 MW; 75A367672732CEB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
Locusta migratoria (Migratory locust).
                                                                                                                                                                                                                                                                   family.";
Comp. Biochem. Physiol. 106C:103-109(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIS, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conus purpurascens (Purple cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.1%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.9%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA; 1145 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVPLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVPTFTP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=41690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leu-contryphan-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olivera B.M.;
                                                                                                                                                       IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEOUENCE,
                                                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \frac{\text{COW2}}{\text{P58785}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COW2_CONPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPERMINE SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECIAL SPECI
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Freund R., Kadenbach B.;
"Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
Bur. J. Blochem. 22::1111-1116(1994).
-!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                            01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last amnotation update)
01-0CT-1994 (Rel. 30, Last annotation update)
Cytochrome c oxidase polypeptide VIc (EC 1.9.3.1) (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Actinopterygii, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.8%; Score 15; DB 1; Length 10; 75.0%; Pred. No. 4.5e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 1; Length 10;
Pred. No. 4.5e+03;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLUTAR LOCATION: Mitochondrial inner membrane PIR; S43630; S43630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA; 977 MW; E11B40769DC772DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase, Inner membrane, Mitochondrion.
NON TER 10 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1990 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 1 (Fragment).
10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial electron transport
                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
MEDLINE=94237150; PubMed=8181469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Query Match
Best Local Similarity 75.vv.,
Best Local Similarity 75.vv.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 37.5
nes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ISVPLSVP 9
```

```
-i-TISSUE SPECIFICITY: Skin.
-i- MASS SPECIFOMETRY: MW=809.2; METHOD=MALDI.
GO; 00005576; C:extracellular; NAS.
GO; GO:0045986; P:negative regulation of smooth muscle contra. .; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Myoactive peptide. Increases the amplitude and frequency of spontaneous contractions and tonus of hindgut muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen T.B., Orr D.F., Shaw C.; "Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural characterization, pharmacological activity and cloning of precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muren J.E., Naessel D.R.;
"Seven tachykinin-related peptides isolated from the brain of "
madeira cockroach; evidence for tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea,
Blaberidae, Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1; Length 7;
Pred. No. 1.4e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA; 794 MW; 7772D37DC7776350 CRC64;
                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tryptophyllin-l (PdT-1).
Pachymedusa dacnicolor (Giant mexican leaf frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Leuchykinin-related peptide 7 (LemTRP 7).
Leucophaea maderae (Madeira cockroach)
                                                                                                                                                                                                                                         Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amphibian defense peptide; Amidation; Hydro
MOD RES 3 3 HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97269266; PubMed=9114447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phyllomedusinae; Pachymedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides 18:7-15(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
VPLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=75988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PAWVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6988;
                                                              1 VXLSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRP7_LEUMA
P81739;
                                                                                                                                                                                                                                     PACDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isoforms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
                                                                                                                                                                                               TPFY PACDA
ID TPFY PACI
AC P83455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
TRP7_LEUMA
DD TRP3 59
DT 30-MAY.
DT 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF 10-MAY.
DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                            à
                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
"Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.";
FEBS Lett. 261:397-401 (1390).
-!- FUNCTION: Myoactive peptide. Stimulates the contraction of the
oviduct and foregut.
-!- SUBCLIDIAR LOCATION: Serveted.
-!- SUBCLIDIAR LOCATION: Serveted.
-!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
PIR; SO8266; ECLQ2M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown protein is: 4.4, its MW is: 49 kDa.
SWISS-2DPAGE; P30088; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neopeera, Orthoperoidea, Orthoptera, Caelifera, Acridomorpha, Acridoidea, Acrididae, Oedipodinae, Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Plasma;
MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 10) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.8%; Score 15; DB 1; Length 10; 100.0%; Pred. No. 4.5e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15; DB 1; Length 10;
Pred. No. 4.5e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 10 10 10 AMIDATION.
10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;
                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Locustatachykinin II (TK-II).
                                                                                                 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA
                                                                                                                                                                                                                                                                                         Locusta migratoria (Migratory locust)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90184489; PubMed=2311766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PLS 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 PLS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UPA2 HUMAN P30088;
                                                                                             LOCMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                P16224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
UPA2 HUMAN
AD PRA2 HUMAN
DT 01-APR
DT 11-APR
DE UNKNOW
OC HUMEN SIGUEN
RR 11]
RR 11]
RR 11SUBER
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SARCHAS
RA SA
                        RESULT 6
TKL2_LOCMI
ID TKL2_L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNSURE
```

Matches

à g

ID DAAC DD DAA

ö

Gaps

; 0

 $^{\text{the}}$ 

Matches

```
Biol. Chem. 262:15821-15824(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U=U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THUOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P80975;
                                                              REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
COXE_THUOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
     REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Litoria rubella (Desert tree frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura; Neobatrachia, Hyloidea, Hylidae;
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88058932; PubMed-3680228;
Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Invertebrate vasopressin/oxytocin homologs. Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arg-conopressin S.
Conus striatus (Striated cone).

Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptides from Conus geographus and Conus straitus venoms.";
                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%; Score 13; DB 1; Length 6; 66.7%; Pred. No. 1.4e+05; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                 Tachykinin; Neuropeptide; Amidation.
MOD RES 10 10 AMIDATION.
SEQÜENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 A AMIDATION.
6 AA; 792 MW; 6683704772C9A000 CRC64;
                                                                                                                                                                                                                                Score 14; DB 1; 1
Pred. No. 6.7e+03;
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Brain.
-!- MASS SPECIFICITY: Brain.
-!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 09, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA
                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aust. J. Chem. 52:639-645(1999).
--- SUBCELLIATA LOGATION: Secreted.
--- TISSUB SPECIFICITY: Skin.
Amphibian defense Peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                          25.0%;
                                                                                                                                                                                                                                                        Local Similarity 75.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Skin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                               4 VPLS 7
                                                                                                                                                                                                                                                                                                                                                                                                  1 VPAS 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VPI 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LITRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONO CONST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rubella."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P05487:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONO_CONST
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0000 X F 8
                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPITE STATE OF SPITE SO SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE SPITE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thunnus obesus (Bigeye tuna).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Heart;
MEDLINE=97454201; PubMed=9310366;
MEDLINE=97454201; FubMed=9310366;
MEDLINE=97454201; FubMed=9310366;
MEDLINE=97454201; FubMed=9310366;
MEDLINE=97454201; FubMed=9310366;
MEDLINE=9745451; FubMed=9310366;
MThe subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liver.",
Bur. J. Biochem. 248:99-103(1997).
-!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
mitochondrial electron transport.
                     Gray W.R., Olivera B.M., Cruz L.J.;

T "Peptide toxins from venomous Conus snails.";

L Annu. Rev. Biochem. 57:665-700 (1988).

-!- FUNCTION: Targets vasopressin-oxytocin related receptors.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECTRICITY: Expressed by the venom duct.

-!- TISSUE SPECTRICITY: Expressed by the venom duct.

-!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

R PIR; B28495; B28495.

R InterPro; IPR000981; Neurhyp_horm.

R PROSITE; PS00204; Neurhyp_horm.

R PROSITE; PS00204; NeUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
-!- SIMILARITY: Belongs to the cytochrome c oxidase VIa family.
PIR; S77984; S77984.
InterPro; IPR001349; COX6A.
PROSITE; PS01329; COX6A; PARTIAL.
Oxidoreductase; Inner membrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Cytochrome c oxidase polypeptide VIa (EC 1.9.3.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.2%; Score 13; DB 1; Length 9; 60.0%; Pred. No. 1.4e+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13; DB 1; Length 9;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  9 9 AMIDATION.
9 AA; 1031 MW; 17EB176EB4540050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
MEDLINE=89024586; PubMed=3052286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 60.0 1es 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            60
```

```
SEQUENCE
                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                        RESULT 15
ALL6_CYDPO
     Matches
                                                  g
                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                  TISSUE-Heart, and Liver;
Freund R., Kadenbach B.;
Submitted (MAR-1994) to Swiss-Prot.
Submitted (MAR-1994) to Swiss-Prot.
-!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome c + 2 H(2)O.
-!- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
Oxidoreductase; Mitochondrion.
NON_TER 10 10
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95380343; PubMed=7651886; Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S., Grautels K., van Leuven F., de Loof A.; Identification, characterization, and immunological localization of a novel myotropic neuropeptide in the Colorado potato beetle, Leptinotarsa deceminata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides 16:365-374(1995).
-!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
                                                                       01-007.

01-007-1994 (Rel. 30, Created)

01-00T-1994 (Rel. 30, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)

(Fragment).

Ovis arises (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

NOBL TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
Leptinotarsa decemineata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neophera; Endopterygota; Coleoptera; Polyphaga; Chrysomelidae; Chrysomelini; Leptinotarsa.
Chrysomelini; Leptinotarsa.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 13; DB 1; Length 10;
Pred. No. 1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                                                         10 AA; 1027 MW; C4E95CA33DC7633D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
6DD73768745B5DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 1;
Pred. No. 1.4e+05;
                                                            10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 705 MW;
                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide, Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, AND SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAKTP 9
PEFVP
                                                            COXO SHEEP
P80337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
MNP1 LEPDE
ID MNP1 LEPDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oviduct
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P42984;
                                               SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                    RESULT 13
                                              COXO
                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

Best Local Similarity

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tortricoidea; Tortricoidea; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).

Peptides 18:1301-1309(1997).

Neuropeptide; Amidation.

MOD RES

**AMIDATION.**
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA; 936 MW; 0B2879C45B573767 CRC64;
     0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 1; I
Pred. No. 1.4e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLG_CYDPO STANDARD; PRT; 8 AA. P82157; 8 AA. P82157; 8 AA. P82157; 8 AA. B82157; 8 AA
     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: September 5, 2004, 11:33:40 Job time : 14 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Larva;
MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.73
Since 2; Conservative
2; Conservative
                                                                                                                                                                      ||:
5 PLA 7
                                                                                                       5 PLS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cydiastatin 6.
```

This Page Blank (uspto)

```
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   035953
                                                                                September 5, 2004, 11:30:23; Search time 57 Seconds (without alignments) 55.354 Million cell updates/sec
                                                                                                                                                                                                                                                                                      1443
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_organelle:*
sp_phage:*
                                                                                                                                             US-09-761-636A-13
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rodent: *
                                                                                                                                                                            1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp plant: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_virus:*
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0.0.0
                                                                                                                                                             Perfect score:
Sequence:
                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                    Searched:
                                                                                   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		O33933 MUSCUIU	085598 molonev mur		O85619 molonev mur	OS6140 streptococc	O7wng2 escherichia	O9v4x6 homo sanien	O7x6a3 zea mays su	096041 nenothera h	O7v0i8 zea mays su	039957 hepatitis q	015898 homo sanien	002831 orvetolagus	O9trv3 sus sp. ins	OSavd3 ovine resni	Q8ay15 carassius a
SUMMARIES	ID	035663	55555	085598	Q85563	085619	056140	O7WUG2	09Y4X6	07X6A3	096041	Q7Y018	039957	015898	002831	O9TRY3	080VD3	QBAYLS
	DB	-	1	15	15	15	7	N	4	10	80	10	12	4	9	9	12	13
	Query Match Length DB	-	•	10	10	10	æ	10	8	σ	10	10	10	<b>6</b> 0	œ	60	σ	σ
æ	Query Match	35 7		35.7	35.7	35.7	33.9	33.9	30.4	30.4	30.4	30.4	30.4	28.6	28.6	28.6	28.6	28.6
	Score	200	1	20	20	20	19	19	17	17	17	17	17	16	16	16	16	16
	Result No.		•	7	æ	4	S	y	7	80	6	10	11	12	13	14	15	16

QBaum? carassius a QBspn8 macaca mula QBspn8 macaca mula QB5az9 pyrrhobryum Q94166 pinus taeda O42564 fugu rubrip	Q915w6 liberibacte Q8x4e5 escherichia Q07624 rous sarcom Q9x3x1 prochloroco			Q8mbb7 merremia ae Q8s154 aeonium haw P83091 spinacia ol O90347 hepatitis g Q8jv78 polyomaviru	Ogruul cynops pyrr Q67113 influenzavi Q8kpx4 microcystis Q49334 mycoplasma	O32560 escherichia Q8iub8 homo sapien Q8wfr5 diadema pau
13 Q8AUM7 6 Q8SPN8 8 Q85AZ9 10 Q94IS6 13 O42564	2 Q9L5W6 16 Q8X4E5 15 Q07624 2 Q9X3K1		0	aa	13 Q9PRU1 12 Q67113 2 Q8KPX4 2 Q49534	2 032560 4 QBIUBB 8 Q8WFR5
66668	.8 10 .0 7 .0 8	0000		00000	.0 10 .2 7 .2 8 .2 8	u'u'u'
00000	15 26 15 26 14 25 14 25	14 25 14 25 14 25 14 25	14 25 14 25 14 25 14 25		14 25 13 23 13 23 13 23	13 23 13 23 13 23
113 118 20 21	22 24 25	2 2 2 5 2 8 7 6	33 33 33 33	\$6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	8 4 4 4 0 1 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	44 44 55 44 55 45 45 45 45 45 45 45 45 4

ú	
H	
z	
ı	
Σ	
z	
J	
ᅼ	
4	
₹	

```
STRAIN=RIII;
MEDLINE=97442476; PubMed=9295353;
MEDLINE=97442476; PubMed=9295353;
MEDLINE=97442476; PubMed=9295353;
MEDLINE=97442476; PubMed=9295353;
MAILERIALIVE splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
Mol. Chem. 272:24008-24015(1997).
EMBL; U97672; AAB80914.1;
MGD; MGI:103169; Scn8a.
GO; GO:0007628; P:adult walking behavior; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                               01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
SCNBA.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           35.7%; Score 20; DB 11; Length 9; 80.0%; Pred. No. 1e+06; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;
   9 A.A.
                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seqn
01-OCT-2003 (TrEMBLrel. 25. Last amma
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||:
1 VPLSL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VPLSV 8
                                                                                                                                                                                                                                                                                                                                                                         Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

RESULT 2 Q85598

; 0

```
STRAIN=ST11;
MEDLINE=95047254; PubMed=7958782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö7WUG2;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
ThpIS1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                         Q56140;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STP6 protein (Fragment). STP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                               NCBI_TaxID=11801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                           7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1308;
                                                                                                                                                                                                                                                                                                 4 STPC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid p541
                                              (Fragment).
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                              Q56140
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
Q7WUG2
                                                                                                                                                                                                                                                                                                                                      RESULT 5
Q56140
                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS OF DIT
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]—
BEDUINE-82196891; PubMed-6281735;
DONOGHUE D.JO., Hunter T.,
"A generalized method of subcloning DNA fragments by restriction site reconstruction. Application to sequencing the amino-terminal region of the transforming gene of dazdar murine sarcoma virus.";
Nucleic Acids Res. 10:2549-2564(1982).
                                                                                                                              MEDLINE=83164305; PubMed=6300424; MEDLINE=83164305; PubMed=6300424; Pondoque D.J., Hunter T.; Pondoque D.J., Hunter T.; Percombination junctions of variants of Moloney murine sarcom virus: Generation and divergence of a mammalian transforming gene."; J. Virol. 45:607-617[1983]. EMBL; K03105; AA446492.1; -. NON TER 10 10 10 SEQÜENCE 10 AA; 1081 MW; 7BECFCBEA771BSA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=83164305; PubMed=6300424; Donoghue D.J., Hunter T.; Donoghue D.J., Hunter T.; Recombination junctions of variants of Moloney murine sarcom virus: Generation and divergence of a mammalian transforming gene."; J. Virol. 45:607-617(1983). BMBL; K03105; AAA46491.1; -. NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o;
          Q85599;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NCV-1996 (TrEMBLrel.) 19, Last annotation update)
Moloney murine sarcoma virus (Strain HT1) env/mos 5' junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%; Score 20; DB 15; Length 10; 75.0%; Pred. No. 3.8e+03; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                   Score 20; DB 15; Length 10;
Pred. No. 3.8e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses, Retroid viruses, Retroviridae, Gammaretrovirus.
NCBI_TaxID=11801;
                                                                                        Viruses; Retroid viruses; Retroviridae; Gammaretrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 10 10 10
SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Env-mos fusion protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                        10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moloney murine leukemia virus.
                                                                                 Moloney murine leukemia virus.
                                                                                                                                                                                                                                                   35.7%;
75.0%;
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 STPC 7
                                                                       (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q85619
Q85619;
                                                                                                                                                                                                                                                                                                                                                                                       Q85563
Q85563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      085619
                                                                                                                                                                                                                                                                                                                                                                            085563
                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Constable A., Mollet B.;
"Isolation and characterisation of promoter regions from Streptococcus thermophilus.";
FEMS Microbiol. Lett. 122:85-90(1994).
EMBL; X78210; CAA55045.1; -.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89164305; PubMed-6300424;
Donoghue D.J., Hunter T.;
The second ination junctions of variants of Moloney murine sarcom virus:
"Recombination junctions of variants of Moloney murine sarcom virus:
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617[1983).
BEMBL; K03108; ARA46594.1; -.
NON_TER 10 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
MOI-DBC-2001 (TrEMBLrel. 19, Last annotation update)
MOIORRY murine sarcoma virus (Strain m1) env/mos 5' junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.7%; Score 20; DB 15; Length 10; 75.0%; Pred. No. 3.8e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.9%; Score 19; DB 2; Length 8; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus thermophilus.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                    Moloney murine leukemia virus.
Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQÜENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
```

```
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=94019250; PubMed=8413195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7.
Loca 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oenothera mitochondria.";
Mol. Gen. Genet. 240:445-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isoamylase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 VPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CIS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CIS 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schuster W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003
                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7Y0I8
Q7Y0I8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 096041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
Q7Y018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      096041
                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCOCCOS ON THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-20108806; PubMed=10640831;
Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Schroth A., Bodem J., Royer-Pokora B.;
"Genomic structure, alternative transcripts and chromosome location of the human Lim domann binding protein gene LDB1.";
Cytogenet. Cell Genet. 87:119-124(1999).
EMBL; AJ243097; CAB45408.1;
MANY TER
                                                                                                                                                                                         Miriagou V., Tzouvelekis L.S., Villa L., Lebessi B., Vatopoulos A.C., Caratroli A., Tzelepi B.;
"Antibiotic Resistance Region of an IncN Plasmid Carrying an Integron-Located blavIM-1-Metallo-b-Lactamase Gene and a Novel CMY-Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays subsp. mays (maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Psprmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4578;
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
VOCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 57.1%; Pred. No. 5.8e+03; Similarity 57.1%; Pred. No. 5.8e+03; 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                        Cephalosporinase Gene.";
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY339625; AAQ16673.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%; Score 17; DB 4; Length 8; 60.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                       10 10 10
10 AA; 991 MW; 882D57A5B045A2D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Nuclear LIM interactor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07X6A3;
01-OCT-2003 (TrEMBLrel. 25, 0
01-OCT-2003 (TrEMBLrel. 25, 1
01-OCT-2003 (TrEMBLrel. 25, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoamylase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVPLSVP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                   [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | |: | |
SVSISCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MŠVGĆ 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y4X6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7X6A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
07X6A3
1D 07X6A3
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 01-0
DT 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
ó:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, Myrtales, Onagraceae, Oenothera.
STRAIN=cv. 38-11, and cv. A632;
Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
Buckler E.S. IV.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Ribosomal protein gene rpl5 is cotranscribed with the nad3 gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays subsp. mays (maize).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                           30.4%; Score 17; DB 10; Length 9; 66.7%; Pred. No. 1e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%; Score 17; DB 8; Length 10; 100.0%; Pred. No. 1.4e+04; ive 0; Mismatches 0; Indels
                                                                            "Dissection of maize starch production by candidate gene association.";
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY290305; AAP45331.1; -.
EMBL; AY290311; AAP45337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 10 AA; 1097 MW; 723067B0476DD9CB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) NADH-ubiquinone oxidoreductase subunit 3 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                      9 AA; 976 MW; DF9BCEA76736C6DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oenothera bertiana (Bertero's evening primrose).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Gen. Genet. 240 445-449 (1993).

EMBL, X69553; CA449285.1; --
GO; GO:0005739; C:mticchondrion; IEA.

Mitochondrion; Ubiquinone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
```

; 0

Gaps

.; 0

```
MEDLINE=92049376; PubMed=1719383;
Shimasaki S., Gao L., Shimonaka M., Ling N.;
"Isolation and molecular cloning of insulin-like growth factor-binding
protein-6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Byidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996)

EMBL; S83371; AAD14433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9826;
                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUM-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pro alpha 1 type III collagen protein (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukayacia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(11995).

EMBL; i32078; AAA73888.1; -.

NON TER 8

SEQUENCE 8 AA, 938 MW; 34A415B0477B45BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-96377339; PubMed-8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.6%; Score 16; DB 6; Length 8; 100.0%; Pred. No. 1e+06; Live 0; Mismatches 0; Indels
                                                                                                                                                          1; Indels
                                                                                                                          Query Match 28.6%; Score 16; DB 4; Length 8; Best Local Similarity 60.0%; Pred. No. 1e+06; Matches 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 1
8 AA; 1028 MW; B859C7272EA77371 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;
                                                                                                                                                                                                                                                                                                   8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Endocrinol. 5:938-948(1991).

NON TER 8

SEQUENCE 8 AA, 850 MW, 9FB2CE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luv...
2; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                         3 SVPLS 7
                                                                                                                                                                                                                     SYPIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 PC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vuorio E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9TRY3
                                                                                                                                                                                                                                                                    RESULT 13
002831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9TRY3
    RT RET DE LET SO ETT SO
                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                     ID
DTTDDTTDDTT
DDTTRN
DDTTRN
RRX
RRX
RRY
RRT
RRT
RRT
RRT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
Caskey C.T.H.;
                                                                                                                                                                                                                                                                                                                                                                           039957;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
El protein (Fragment).
Hepatitis GB virus C.
Hepatitis GB virus C.
GBV-C/HGY group.
NCLUS-S9839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith D.B., Cuceanu N., Davidson'F., Jarvis L.M., Mokili J.L.,
Hamid S., Ludlam C.A., Simmonds P.;
"Discrimination of hepatides G virus/GBV-C geographical variants by
analysis of the 5' non-coding region.";
J. Gen. Virol. 78:1533-1542(1997).

BMBL, AP003175; AAC57986.1;
10
10
10
10
                                STRAIN=cv. K144;
Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
Buckler E.S. IV.;
"Dissection of maize starch production by candidate gene
association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                        Score 17; DB 10; Length 10;
Pred. No. 1.4e+04;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.4%; Score 17; DB 12; Length 10; 60.0%; Pred. No. 1.4e+04; ative 2; Mismatches 0; Indels
                                                                                                         Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: AY290360; AAP45386.1; -.
NON_TER 10 10
SEQUENCE 10 AA; 1063 MW; DOFF9BCEA76736C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQÜENCE 10 AA; 1067 MW; CC88FE2727273772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               015898;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(Clone XP6Al1B) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                 10 AA
                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=Ed inburgh haemophiliac;
MEDLINE=97368412; PubMed=9225026;
                                                                                                                                                                                         30.4%;
                                                                                                                                                                       Ouery Match
Best Local Similarity 66.7.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|||
1 MAVPL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 ISVPL 6
                                                                                                                                                                                                                                                       8 VPC 10
                                                                                                                                                                                                                                                                       :||
5 LPC 7
                                                                                                                                                                                                                                                                                                                                                              039957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q15898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
Q15898
                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RN
RP
RA
RT
RT
BT
SQ
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                              ò
```

; 0

Gaps

.. 0

```
ô
                                                                                                        ;
0
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21580659; PubMed=11724134;
Eleraky N.Z., Kania S.A., Potgieter L.N.;
Eleraky N.Z., Kania S.A., Potgieter L.N.;
"The ovine respiratory syncytial virus F gene sequence and its diagnostic application.";
J. Vet. Diagn. Invest. 13:455-461(2001).
ENBL, AF334398; AAL91343.1;
NON TER
SEQUENCE 9 AA; 1154 MW; BB6A3EA764541415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
08QVD3
ID 08QVD3
AC 08QVD3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DN MAIRING PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROPERTION PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.6%; Score 16; DB 12; Length 9; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
Query Match
28.6%; Score 16; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                  9 PC 10
||
6 PC 7
                                                                                                                                                                                            à
                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

Search completed: September 5, 2004, 11:34:44 Job time: 58 secs

임

This Page Blank (uspto)

```
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                 Copyright
```

OM protein - protein search, using sw model

5, 2004, 11:27:12 September on:

2; Search time 63 Seconds (without alignments) 44.849 Million cell updates/sec

US-09-761-636A-13 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 CISVPLSVPC 10 Scoring table: Sequence:

1586107 segs, 282547505 residues Searched:

325896 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

A_Geneseq 29Jan04:* Database

geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2004s:* чик 4 горга |........

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	crip	Aau04532 VEGF base	Aau04533 VEGF base	Aar96138 Protease	Aaw82212 D-NorFES-	Aaw46562 Peptide b	Aar96137 Protease	Aaw82094 D-NorFES-	Aaw46561 Peptide b	Aag73245 Protease	7	Aau00643 Human mem	Adb88786 Membrane	Aau94301 Human nov	Aau94201 Human nov	Aau94811 Human nov	Aau94577 Human nov	Aam50003 Human D40	Human	Aau94696 Human nov	Aau95023 Human nov	Aag73418 Human gen	Aag85638 Saccharom		Abr19062 Human can	Ahr19524 Himan can
SUMMARIES	ΩI	AAU04532	AAU04533	AAR96138	AAW82212	AAW46562	AAR96137	AAW82094	AAW46561	AAG73245	ABU60357	AAU00643	ADB88786	AAU94301	AAU94201	AAU94811	AAU94577	AAM50003	AAU95231	AAU94696	AAU95023	AAG73418	AAG85638	ABG64264	ABR19062	ABR19524
	DB	4	4	N	0	7	~	N	7	4	Ŋ	4	7	Ŋ	Ŋ	ហ	2	5	2	2	S	4	4	2	9	9
	Query Match Length	10	0	o,	σ	6	0	σ	σ	σ	σħ	10	10	σ	10	10	10	10	6	6	6	10	10	10	σ	10
o <del>V</del>	Query	100.0	74.1	64.3	64.3	64.3	58.9	58.9	58.9	58.9	58.9	57.1	57.1	56.2	56.2	56.2	56.2	55.4	53.6	53.6		51.8	51.8		50.0	50.0
	Score	26	41.5	36		36	33	33	33	33		32	32	31.5	31.5	31.5	31.5	31	30	30	30	29	29		28	28
	Result No.	н.	7	e	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abr18877 Human can	Aar74541 Protease	Adc71003 HLA motif	Adc70887 HLA motif	Adc70636 HLA motif	Adc70959 HLA motif	Adc70732 HLA motif	Adc70653 HLA motif	Adc71049 HLA motif	Aap82102 Non-label	Abg34945 Human bon	Abj04424 Stem cell	Aam48672 CXCR4 pep	Aaw12561 SH2 bindi	Abu96540 Human cyt	Aau04529 VEGF base	Aar77368 SH3 bindi	Aag98618 Human cel	Aae05003 Human rel	Aab60620 Human MuM
6 ABR18877	2 AAR74541	7 ADC71003	7 ADC70887	7 ADC70636	7 ADC70959	7 ADC70732	7 ADC70653	7 ADC71049	1 AAP82102	5 ABG34945	5 ABJ04424	5 AAM48672	2 AAW12561	6 ABU96540	4 AAU04529	2 AAR77368	4 AAG98618	4 AAE05003	4 AAB60620
10	<b>6</b> 0	σ	σ	10	10	10	10	10	σ	σ	σ	σ	10	7	σ	10	10	9	9
50.0	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	46.4	46.4	46.4	46.4	46.4	44.6	44.6	44.6	44.6	42.9	42.9
28	27	27	27	27	27	27	27	27	56	56	56	56	56	25	25	25	25	24	24
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

AAU04532 standard; peptide; 10 AA. VEGF based monocyclic peptide 10. (first entry) 26-SEP-2001 AAU04532; AAU04532 

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

1. .10 /note= "This bond cyclises the peptide" Location/Qualifiers 18-JAN-2001; 2001WO-US001533. Key Disulfide-bond WO200152875-A1 26-JUL-2001

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

Cendron A; Stacker S, Hughes RA, Achen MG,

(LUDW-) LUDWIG INST CANCER RES.

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

residues

```
Characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, archropathy, hemangioma, vascularised malignant or benjus archropathy, hemangioma, vascularised malignant or benjus tractorery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertenaion induced neovascular sequelae, or chronic liver infection. The peptides are also used to medulate vascular permeability in anammal lampa a condition characterised by fluid or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere vasculature. The monomeric and bicyclic peptides are used to interfere vasculature. The monomeric and bicyclic peptides are used to interfere vasculature. The monomeric and bicyclic peptides are used to interfere vasculature. The monomeric and bicyclic peptides are used to interfere vasculature and so used in combination with an anti-inflammatory agent, to treat a
peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with a least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neovascularisation, lymphangiogenesis, psoriasis, tumour, diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 56; DB 4; Length 10; 100.0%; Pred. No. 0.0098; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .9
/note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU04533 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF based monocyclic peptide 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
   HANDER STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE STANKE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

```
The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta method of producing a monomeric monocyclic peptide by a measuring beta peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Co peptides, and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Co characterised by angiogenesis in a mammal with a condition characterised by angiogenesis neovascularisation or lymphangiogenesis.

Co resprovascular accident, post-angioplasty restenosis, head, heat or cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoned cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological acciding period are used to interfere with at least one biological acciding atthritis, psoriasis and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .3
/label= C1
/note= "the two conformation determining regions C1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "peptide comprising a protease recognition site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fluorogenic substrate, fluorophore, protease activity, assay, visible fluorescence, in situ detection, frozen tissue section, histology, arthritis, emphysema, thrombosis, cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease substrate peptide with fluorophore at each terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "labelled by donor fluorophore (F1)
carboxytetramethylrhodamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.1%; Score 41.5; DB 4; Length 9; 90.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angstroms of each other"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                   Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR96138 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 90..
Best Son 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CISVPLSVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CISVPL-VPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
18-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR96138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR96138
f H 	imes 0 	                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE STATE STATES OF THE STATES
```

```
The present sequence is a specific example of a fluorogenic substrate for detecting activity of a protease. The substrate agrees with the generic formula (S1)n-(G1F1)-P-C2(P2)-(S2)k in which a peptide P of 2-8 amino acids comprising a recognition site for the protease is flanked by conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and C2 are labelled by fluorophore groups (F1 and P2, respectively) positioned within 100 angstroms of each other. Additional peptide spacers of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or 1). Fluorogenic substrates corresponding to the generic formula are used
                                    /note= "the two conformation determining regions C1 and C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100 angstroms of each other"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1). Fluorogenic substrates corresponding community of the specimens, esp. in frozen to detect or localise proteases in biological specimens, esp. in frozen tissue sections or to monitor protease activity in stored reagents. Changes in protease activity are associated with e.g. arthritis, emphysema, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
                                                                                                                                            /note= "labelled by acceptor fluorophore F2 rhodamine X acetamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protease activity, fluorphore, detection, fluorogenic, cellular uptake, conformation change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New fluorogenic peptide(s) with fluorophore at each terminus - for detecting protease(s) in biological samples, emit intense visible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-NorFES-A protease inhibitor peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 31; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW82212 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                  95WO-US013936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                    94US-00331383
3. .9
/label= C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fluorescence when cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komoriya A, Packard BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONCO-) ONCOIMMUNIN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::|:|:|
AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-239512/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                  27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1994;
                                                                                                                                                                                                                                                  WO9613607-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9837226-A1
                                                                                                                                                                                                                                                                                                 09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW82212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
```

· 0

à g

```
AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, polysaccharides, proteins, peptides, lipids, phopholipids, glycolipids, glycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to a molecule can be used to enhance uptake by cells. The composition is composed of P = peptide comprising a protease binding site for the protease, F1, F2 peptides = fluorophores where F1 is attached to the amino terminal amino acid and S1, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal acid, and S2, when present, is attached to the amino terminal acid, and S2, when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease; protease indicator; fluorescent signal;
                                                                                                                                                                          orogenic compositions - containing 2 fluorophores separated by a comprising a protease binding site, used for detecting protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fluorogenic substrates for protease determination - having two closely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.3%; Score 36; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide backbone of a protease indicator.
                                                                                                                                                                                                                                       Example 1; Page 52; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW46562 standard; peptide; 9 AA.
                             98WO-US003000.
                                                         97US-00802981.
                                                                                                                                                                           New fluorogenic compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease binding site; protedetection; protedetection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00549008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-00331383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                  BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Komoriya A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ONCO-) ONCOIMMUNIN INC
                                                                                     (ONCO-) ONCOIMMUNIN INC
                                                                                                                  Packard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SVPLSVPC 10
                                                                                                                                               WPI; 1998-467579/40.
                                                                                                                                                                                                          activity in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-158345/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|:|:|
AIPMSIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
                             20-FEB-1998;
                                                         20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-OCT-1994;
                                                                                                                  Komoriya A,
27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS5714342-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Packard BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW46562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

0

```
The present sequence is a specific example of a fluorogenic substrate for detecting activity of a protease. The substrate agrees with the generic formula (S1)n-C1(F1)-FC2(F2)-(S2)k in which a peptide p of 2-8 amino acids comprising a recognition site for the protease is flanked by conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and C2 are labelled by fluorophore groups (F1 and F2, respectively) positioned within 100 angstroms of each other. Additional peptide spacers of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or 1). Fluorogenic substrates corresponding to the generic formula are used to detect or localise proteases in biological specimens, esp. in frozen tissue sections or to monitor protease activity in stored reagents. Changes in protease activity are associated with e.g. arthritis, embhysems, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease activity; fluorphore; detection; fluorogenic; cellular uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Asp residue is modified by the presence of where F1 is the donor fluorophore 5'-carboxytetramethylrhodamine (C2211)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Cys residue is modified by the presence of
                                                                                                                                                                                                                                                                                                                                                   New fluorogenic peptide(s) with fluorophore at each terminus - for detecting protease(s) in biological samples, emit intense visible fluorescence when cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%; Score 33; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-NorFES-A protease inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Norleucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 31; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW82094 standard; peptide; 9 AA.
                                                                                                                                 95WO-US013936
                                                                                                                                                                             94US-00331383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.00,
hea 4; Conservative
  acetamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                 Packard BS;
                                                                                                                                                                                                                      (ONCO-) ONCOIMMUNIN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conformation change.
                                                                                                                                                                                                                                                                                                          WPI; 1996-239512/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    emphysema, thrombo
correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIPXSIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                             WO9613607-A1
                                                                                                                                 27-OCT-1995;
                                                                                                                                                                             28-OCT-1994;
                                                                                                                                                                                                                                                                 Komoriya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW82094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW82094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present peptide contains a protease binding site. It is used to produce novel reagents whose fluorescence increases in the presence of produce novel reagents whose fluorescence increases in the presence of particular proteases. These fluorescent signal at a visible wavelength when they are digested by a protease. The fluorogenic indicators have the general formula: F1-C1-P-C2-F2 | (G1)n (G2)k where: P is a peptide general formula: F1-C1-P-C2-F2 | (G1)n (G2)k where: P is a peptide containing a protease binding site e.g. ANW46520-53, AAW46550. F1 and F2 are fluorophores. S1 and S2 are peptide spacers e.g. AAW46550. F1 and F2 are fluorophores adjacent to bend into the composition which positions the fluorophores adjacent to each other with a separation of less than 100 Angstrom. When n is 1, S1 is joined to the terminal alpha -amino group of C1 by a peptide bond, and when k is 1, S2 is joined to the terminal carboxy group of C2 by a cativity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /______the two conformation determining regions C1 and C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100 angstroms of each other"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "the two conformation determining regions C1 and C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100 angstroms of each other"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "labelled by acceptor fluorophore F2 rhodamine X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "peptide comprising a protease recognition site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fluorogenic substrate; fluorophore; protease activity; assay; visible fluorescence; in situ detection; frozen tissue section; histology; arthritis; emphysema; thrombosis; cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease substrate peptide with fluorophore at each terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "labelled by donor fluorophore (F1)
carboxytetramethylrhodamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 9;
Pred. No. 1.4e+06;
4; Mismatches 0; Indels
spaced fluorophores flanking protease binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                          fluorescence indicating protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR96137 standard; peptide; 9 AA.
                                           Example 1; Col 23; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .3
|abel= C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .3
/label= C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::|:|:|
2 AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR96137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
```

ò g ô

Gaps

.;

E

 $\mathbf{F}_2$ 

```
·
0
                                                                                                                                                                                                                                                                                                                                AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, polysaccharides, proteins, peptides, lipids, phopholipids, glycolipids, glycoproteins, steroids or polywners. In addition, attachment of a hydrophobic group to amolecule can be used to enhance uptake by cells. The composition is composed of P = peptide comprising a protease binding site for the protease, F1, F2 peptides = fluorophores where F1 is attached to the amino terminal amino acid and F2 is attached to the carboxyl terminal amino acid and S1, S2 peptides e when present, are peptide spacers where present, is attached to the amino terminal acid, and S2, when present, is attached to the amino terminal acid, and S2, when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protease binding site; protease; protease indicator; fluorescent signal;
                                                                                                                                                                                                                                               New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
where F2 is the acceptor fluorophore rhodamine X acetamide (R492)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2; Length 9;
Pred. No. 1.4e+06;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide backbone of a protease indicator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Nle
/note= "Norleucine"
                                                                                                                                                                                                                                                                                                       Disclosure; Page 10; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW46561 standard; peptide; 9 AA.
                                                                                                    98WO-US003000
                                                                                                                                97US-00802981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection; protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00549008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                            (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                         Komoriya A, Packard BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SVPLSVPC 10
                                                                                                                                                                                                                                                                             activity in samples.
                                                                                                                                                                                                                  WPI; 1998-467579/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::| |:||
AIPXSIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Modified-site
                                                                                                                                20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1995;
                                                                                                    20-FEB-1998;
                                           WO9837226-A1
                                                                       27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5714342-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW46561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
The present peptide contains a protease binding site. It is used to produce novel reagents whose fluorescence increases in the presence of produce novel reagents whose fluorescence increases in the presence of produce a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The fluorogenic indicators have the general formula: F1-C1-P-C2-F2 | (S1)n (S2)k where: P is a peptide containing a protease binding site e Q. AMW46520-53, AAMW4650. F1 and F2 are fluorophores. S1 and S2 are peptide spacers e.g. AAW46550. F1 and F2 are fluorophores sition which postitions the fluorophores adjacent to bend into the composition which postitions the fluorophores adjacent to cach other with a separation of less than 100 Angstrom. When n is 1, S1 is joined to the terminal alpha -amino group of C1 by a peptide bond, and when k is 1, S2 is joined to the terminal carboxy group of C2 by a cachity in a biological sample. The sample is contacted with the activity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                    Fluorogenic substrates for protease determination - having two closely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease detection; peptide cleavage; enzyme activity, fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.9%; Score 33; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                     spaced fluorophores flanking protease binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "modified by fluorophore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "modified by fluorophore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fluorescence indicating protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                      Example 1; Col 23; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG73245 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease indicator peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= OTHER
              94US-00331383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2000; 2000WO-US024882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SVPLSVPC 10
                                                                                                                    WPI; 1998-158345/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200118238-A1
              28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2001.
                                                                                  Packard BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG73245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG73245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Thus invention describes a loyer intractor Computation (relative as induced councils) wherehold describes a loyer intractor computation (the same species muchate acid backbone joining two chromophores of the same species whereby the chromophores form an H-dimer resulting in quenching of the curcles that the chromophore of a change in the absorbance of the chromophore, a decrease in fluorescence or a change in the absorbance of the chromophore, a decrease in fluorescence or a change in absorbance indicates that the indicator is fluorescence or a change in absorbance indicates, that the indicator is classes the protease a mammalian, yeast or insect cell. The composition bears a cluorescence or a change in absorbance indicator is attached to a solid cluorencearboxylic group, bearyloxycarbonyl Marby (Mar), Horomoposition bears a chydrophobic group such as Fact, 9-fluorencearboxylic group, bearyloxycarbonyl Marby (Mar), Trityl (Trt), 4 methoxylic group, bearyloxycarbonyl Marby) (Mar), Mestlylene-2-sulphonyl (Mar), Trityl (Trt), 4 methoxylic group, bearyloxycarbonyl Marby (Mar), Mestlylene-2-sulphonyl (Mar), 4 methoxylic group, bearyloxycarbonyl Marby, 4 methoxylic group, bearyloxycarbonyl Marby, 6 methoxylic group, bearyloxycarbonyl Marby, 6 methoxylic group, bearyloxycarbonyl Marby, 4 methoxylic group, 6 methoxylic group, bearyloxycarbonyl Marby, 6 methoxylic group, 6 minuted adherent cells), a biological sample such as tissue, blood, urine, saliva, lymph, or biopsy cromposition of minuted adherent cells, a procease activity in a minuted activity and a minuted adherent and minuted adherent and an early determination of procease activity, Marbolosic group and are assily detected in biological samp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane translocating peptide; MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
                                                                                                                                                                       This invention describes a novel indicator composition (referred as homo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection of protease activity. ABU60357-ABU60477 represent peptides use to illustrate the method described in the disclosure of the invention
                                     Indicator composition comprising polypeptide or nucleic acid backbone joining two same chromophores resulting in quenching of fluorescence of/change in absorbance of chromophores, useful for detecting protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%; Score 33; DB 5; Length 9; 50.0%; Pred. No. 1.4e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human membrane translocating peptide (MTLP) #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU00643 standard; peptide; 10 AA.
                                                                                                                                    Example 2; Page 15; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVPLSVPC 10
   WPI; 2002-698548/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | | | | | | | AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU00643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                  activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU00643
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "F2, where F2 is an acceptor fluorophore rhodamine X acetamide (R492)"
                                                                                                                                                                                                                                                                                                    used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metastasis, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide is clasved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention
                                                                                                                                                  New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue
                                                                                                                                                                                                                                                                                    present invention describes fluorogenic compositions which can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease, indicator, chromophore, H-dimer, fluorescence, absorbance, nuclease, screening, fluorophore, substrate cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "F1, where F1 is a donor fluorophore 5'-
carbocytetramethylrhodamine (C2211)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.9%; Score 33; DB 4; Length 9; 50.0%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D-NorFES-A protease inhibitor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "norleucine"
                                                                                                                                                                                                                                                Example 2; Page 53; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU60357 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DEC-2000; 2000US-00747287,
 99US-00394019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-DEC-2001; 2001WO-US049781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50...
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Packard BS, Komoriya A;
                                                                          Packard BS;
                                     (ONCO-) ONCOIMMUNIN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                WPI; 2001-389573/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AIPXSIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200261038-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-APR-2003
                                                                          Komoriya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU60357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU60357
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

ö

Gaps

.

```
The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the invention is a transcription factor or a protein that activates a transcription factor or a protein that activates of transcription and activator of transcription 3. NK appasaby: T plus communit, S-myc prote-oncogene, myc related, NM2-M2, nucleoside to subunit, S-myc prote-oncogene, myc related, NM2-M2, nucleoside concogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CFS precursor, HSP concogene, and p54. The preferred upregulated protein of the invention is selected from clusterin, T-cell surface glycoprotein CFS precursor, HSP concogene, and psycholipase A2 precursor and the mRNA is for a protein selected from the group. The method is useful for increasing or decreasing the level of a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also be used to enhance transport of a drug through the gastrointestimal tract concominant in the protein peptide of the form the drug through the gastrointestimal tract form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the form the 
                                                                                                                                                                                                     Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2El1;
calcium transport protein; cancer; prostate cancer; cytostatic;
chromosome 7q34; chromosome 12q24.1; T cell; B cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human novel protein CaTrF2E11 HLA binding peptide #134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raitano AB, Challita-Eid PM, Faris M, Sa
Levin E, Hubert RS, Ge W, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                     Example 6; Page 51; 147pp; English.
                                                                                               Brayden D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU94301 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-2001; 2001WO-US025782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2000; 2000US-0226329P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                         O'mahony DJ, Byrne D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CLPVLLAAPC 10
                                   (OMAH/) O'MAHONY D J.
                                                                                                                                            WPI; 2003-229409/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200214361-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU94301;
                                                                                                                                                                                                                                                                                               factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU94301
           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a human membrane translocated peptide (MTLP).

MTLPS and their related fragments, motifs, derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer lining the gastrointestinal tract).

Example, an epithelial cell layer lining the gastrointestinal tract) of either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the dentification of MTLPs which retain the functional activity of a full-length MTLP, as a cell-based screen for assaying the functional activity of a MTLP and characterising the properties of a MTLP, for diagnosis of a pathological disorder (by administration of a MTLP-active agent complex or MTLP-active particle complex comprising a diagnostic agent) and for correcting a pathological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 4; Length 10; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Membrane translocating peptide #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB88786 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 11; 42pp; English.
                                                                                                              27-SEP-2000; 2000WO-IB001491
                                                                                                                                                                       99US-0156246P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-APR-2002; 2002WO-IB003866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-2001; 2001US-0281387P. 02-JUL-2001; 2001US-0302591P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CLPVLLAAPC 10
                                                                                                                                                                                                                                                                                                                 Lambkin
                                                                                                                                                                                                                             (OMAH/) O'MAHONY D J
                                                                                                                                                                                                                                                           (LAMB/) LAMBKIN I J.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-300212/31.
N-PSDB; AAS00637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003004646-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10 AA;
WO200127154-A2
                                                                                                                                                                                                                                                                                                                 O'mahony DJ,
                                                                                                                                                                    27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-2003
                                                        19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB88786;
```

Matches

à g

.. 0

Gaps

.; 0

Score 32; DB 7; Length 10; Pred. No. 82; 2; Mismatches 3; Indels

Afar DEH;

Saffran DC,

21-FEB-2002

```
The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7943) gene products in a biological sample from an apacient who has or is suspected of having cancer cancer) comparing the status of sapells in a trivial sample from an individual and (b) comparing the status to the status of 83P2H3 gene individual and (b) comparing the status to the status of 83P2H3 gene individual and (b) comparing the status to the status of 83P2H3 gene individual and (b) comparing the status to the status of 83P2H3 gene comparing the status to the status of 83P2H3 gene comparing the status to the status of 83P2H3 gene comparing the status to the status of 83P2H3 gene comparing antibodise/immune response against 83P2H3 conjugating antibodise/immune response against 83P2H3 computed from the protein, delivering a cytocoxic agent to a cell carried from the protein comprising an antigen-binding region of the antibody, a recombinant protein comprising an antigen-binding region of the heavy and comprises the recombinant protein, a non-human transgenic animal that produces the recombinant protein, a comprises the recombinant protein, a polymucleotide that encodes the monoclonal antibody and inducing an infinite response to a 83P2H3 antibody, and contracting the copy, and contacting the protein comprises a T cell or B cell, respectively. The method is useful for inhibiting the growth of cancer in a biological sample for monitoring the presence of cancer in an individual. The modulator is cancer that expresses 83P2H3. The immune response against 83P2H3 and for detecting the presence of 83P2H3-related protein or polymucleotide in a biological sample from a patient who has or who is suspected of having cancer man the hold is useful for monitoring 83P2H3 monological methodological methodologica and treatment, to detect and quantify 83P3H3 and mutant sequence of 83P2H3-related protein. The present sequence of 83P2H3-related protein, for purifying a 83P2H3-related protein. The present sequence of 83
                                                  Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample.
                                                                                                                                                              Example 11; Page 173; 270pp; English.
WPI; 2002-269179/31
```

Gaps ä 56.2%; Score 31.5; DB 5; Length 9; 60.0%; Pred. No. 1.4e+06; ive 2; Mismatches 1; Indels Query Match
Best Local Similarity 60.v6, Conservative 1 CISVPLSVPC 10 Sequence 9 AA; à

σ |:: || || 1 CLT-PLSFPC 원

AAU94201 standard; peptide; 10 AA. 02-JUL-2002 (first entry) AAU94201; RESULT 14 AAU94201 

Human, human leukocyte antigen; HLA, immunogen; 83P2H3; CaTrF2Ell; calcium transport protein; cancer; prostate cancer; cytostatic; chromosome 7q34; chromosome 12q24.1; T cell; B cell. Human novel protein CaTrF2E11 HLA binding peptide #84.

Homo sapiens

WO200214361-A2.

```
Companie from a patient who has or is suspected or having cancer (especially prostate cancer), comprises: (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) companie, his of included are modulators of 83P2H3 gene individual and (b) companie, his of included are modulators of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 gene function or status, generating antibodise/immune response against 83P2H3 (or related protein Cafrefall whose generating actoroxic agent to a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a non-human transgenic animal that produces the recombinant protein, a single-chain of the anti-83P2H3 antibody, a some non-human transgenic animal that produces the recombinant protein, a single-chain of the anti-83P2H3 antibody, a some of 11ght chains of the anti-83P2H3 antibody, a vector comprising an immune response to a 83P2H3 protein, by providing a 83P2H3 antibody and inducing an immune response to a 83P2H3 protein, by providing a 83P2H3 and contacting the presence of cancer in an individual. The modulator is useful for inhibiting the growth of cancer cells that expresse 83P2H3, for treating an immune response against 83P2H3, and for detecting the treating anner and the vector is useful for reating a patient with a treating anner and the vector is useful for reating a patient with a treating anner and the vector is useful for reating a patient with a treatment, to detect and guantify 83P2H3 and muteant cancer that expresses 83P2H3. The immunological methodologies and treatment, to or polymucleotide in a biological cancer diagnosis, prognosis, imaging antibody is useful in prostate cancer diagnosis, prognosis, imaging an Hisbody is useful in prostate cancer diagnosis, prognosis, imaging all antibody is useful in prostate cancer diagnosis, prognosis, imaging elabering sequence of cancer diagnosis, progno
                                                                                                                                                                                                                                                                                                                                                Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological sample from a patient who has or is suspected of having cancer
                                                                                                                                                                                                                         Afar DEH;
                                                                                                                                                                                                                         Saffran DC,
                                                                                                                                                                                                                         -Eid PM, Faris M, Sa
Ge W, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 11; Page 169; 270pp; English.
                                                                                                                                                                                                                         Challita-Eid PM,
                                                                       17-AUG-2001; 2001WO-US025782
                                                                                                                       17-AUG-2000; 2000US-0226329P
                                                                                                                                                                                                                           Raitano AB, Challita
Levin E, Hubert RS,
                                                                                                                                                                                                                                                                                                WPI; 2002-269179/31.
                                                                                                                                                                         (AGEN-) AGENSYS INC
```

Gaps 1; Score 31.5; DB 5; Length 10; Pred. No. 99; 1; Indels 2; Mismatches 56.2%; 6; Conservative 1 CISVPLSVPC 10 Ouery Match Best Local Similarity Matches δ

Sequence 10 AA;

ä

|:: ||| || CLT-PLSFPC RESULT 15 AAU94811 g

AAU94811 standard; peptide; 10 AA. AAU94811; 7

Gaps

.. H

```
02-JUL-2002 (first entry)
```

Human novel protein CaTrF2E11 HLA binding peptide #394.

Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2B11; calcium transport protein; cancer; prostate cancer; cytostatic; chromosome 7q34; chromosome 12q24.1; T cell; B cell.

Homo sapiens.

WO200214361-A2.

21-FEB-2002

17-AUG-2001; 2001WO-US025782.

17-AUG-2000; 2000US-0226329P

(AGEN-) AGENSYS INC

Raitano AB, Challita-Eid PM, Faris M, Saffran DC, Afar DEH, Levin E, Hubert RS, Ge W, Jakobovits A;

WPI; 2002-269179/31.

Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample.

Example 11; Page 191; 270pp; English.

The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7934) gene products in a biological sample from a patient who has or is uspected of having cancer (sepecially prostate cancer). Comprises: (a) determining the status of (sepecially prostate cancer). Comprises: (a) determining the status of 3P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene cornal sample. Also included are modulators of 83P2H3 gene cornal sample. Also included are modulators of 83P2H3 gene cornal sample. Also included are modulators of 83P2H3 gene produces the status of 102424.1) using identified HLA (human leukocyte antigen) binding peptides derived from the protein, delivering a cytotoxic agent to a cell actived from the protein comprising an antigen-binding ragion of the antibody. The combinant protein comprising an antigen-binding ragion of the antibody. The comprises the recombinant protein, a non-human transgenic animal that produces the recombinant protein, a non-human transgenic animal that produces the recombinant protein, a non-human transgenic animal that produces the recombinant protein, a non-human transgenic animal that produces the recombinant protein, a non-human transgenic animal that produces the recombinant protein, a coll or polynucleotide that encodes the monoclonal antibody and inducing an immune response to a 33P2H3 antibody, a vector comprising a polynucleotide that encodes the monoclonal antibody and inducing an concert that expresses a T cell or B cell, respectively. The method concert that expresses 83P2H3 gene produces in a biological sample for monitoring 83P2H3 gene produces in a biological sample for monitoring the growth of cancer cells that express 83P2H3. For treating a nimmune response against 83P2H3, and for detecting the presence of 83P2H3-related protein or polynucleoside in a biological and treatment, to detect and quantify 83P3H3 method sample from a patient who has o

Sequence 10 AA;

Query Match 56.2%; Score 31.5; DB 5; Length 10; Best Local Similarity 60.0%; Pred. No. 99;

Search completed: September 5, 2004, 11:33:20 Job time : 64 secs

This Page Blank (uspto)

```
(without alignments)
47.737 Million cell updates/sec
                                                                                                                                                                               September 5, 2004, 11:34:49 ; Search time 66 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'cgnz_6'ptodata/2'pubpaa/US07 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US07 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US06 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US06 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US07 NEW PUB.pep:*
'cgnz_6'ptodata/2'pubpaa/PCUS_PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 NEW PUB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 NEW PUB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US09 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US09 NEW PUB.pep:*
'cgnz_6'ptodata/2'pubpaa/US09 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US09 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US09 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 PUBCOMB.pep:*
'cgnz_6'ptodata/2'pubpaa/US08 NEW PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                  OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                US-09-761-636A-13
56
1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 10
                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                   Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 13. Appl	Sequence 14, Appl	; <del>, ,</del>		18	13	71.	Sequence 101. Ann	13	284		560.	794	11221	
SUMMARIES	QI.	US-09-761-636A-13	US-09-761-636A-14	US-09-747-287-1	US-09-874-350A-1	US-09-874-350A-184	US-10-126-845-13	US-10-126-845-71	US-10-116-275-101	US-10-764-235-13	US-09-932-165-284	US-09-932-165-184	US-09-932-165-560	US-09-932-165-794	US-10-154-884B-11221	US-10-363-791-194
	DB	δ	σ	12	12	12	14	14	15	16	10	10	10	10	15	12
	Match Length DB	10	6	σ	6	6	10	10	10	10	9	10	10	10	6	10
* Query	Match	100.0	74.1	58.9	58.9	58.9	57.1	57.1	57.1	57.1	56.2	2.99	56.2	56.2	55.4	55.4
	Score	99	41.5	33	33	33	32	32	32	32	31.5	31.5	31.5	31.5	31	31
Result	No.	Н	C)	m	4	n	9	7	80	9	10	11	12	13	14	15

Sequence 679. App	Sequence 1006. Ap	Sequence 1214, Ap	Sequence 1011, Ap	Sequence 66, Appl	Sequence 11228, A		11254,	11258,		11265,	11275,	11280,	421,		equence 170,		266,	493	Ŋ	m	43	5	112		Sequence 10. Appl	Sequence 21, Appl	Sequence 5, Appli	d)	Sequence 12, Appl
US-09-932-165-679	US-09-932-165-1006	US-09-932-165-1214	US-09-833-245-1011	US-09-756-283A-66	US-10-154-884B-11228	US-10-154-884B-11250	US-10-154-884B-11254	US-10-154-884B-11258	US-10-154-884B-11259	US-10-154-884B-11265	_	US-10-154-884B-11280	US-10-415-014-421	US-10-415-014-537	US-10-415-014-170	-415-014	US-10-415-014-266	US-10-415-014-493	US-10-415-014-583	US-09-852-424-32	US-09-852-424-43	US-10-363-208-21	US-10-154-884B-11276	US-10-154-884B-11287	US-09-761-636A-10	US-09-922-261-21	US-09-866-135-5	US-09-886-135-5	US-09-935-430-12
10	10	10	11	თ	15	15	15	15	15	15	15	15	16	16	16	16	16	16	16	σ	σ	12	15	15	6	δ	6	10	12
6	6	9	10	80	6	9	9	σ	6	Ø.	Q,	Q	σ	σ	10	10	10	10	10	6	6	6	6	Ø.	σ	10	Ŋ	S	σ
53.6	53.6	53.6	51.8	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	46.4	46.4	46.4	46.4	46.4	44.6	44.6	42.9	42.9	42.9
30	30	30	29	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	56	26	56	56	56	25	25	24	24	24
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
RESULT 1
US-09-76-1636A-13

Sequence 13, Application US/09761636A

Patent No. US20020065218A1

GENERAL INPORMATION:
APPLICANT: ACHEN, Marc

APPLICANT: STACKER, Steven

APPLICANT: CRUDROW, Angela

TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

FILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR

CURRENT APPLICATION NUMBER: US/09/761,636A

FRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-01-18

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PatentIn version 3.0

TYPE: PRI

CRENTH: 10

TYPE: PRI

TYPE:
```

1 CISVPLSVPC 10

.,

RESULT 2 US-09-761-636A-14 Sequence 14, Application US/09761636A ; Patent No. US20020065218A1

```
SEQ ID NO 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOMORIYA, AKIRA
APPLICANT: KOMORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.
TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
FILE REFERENCE: 300-946600US
CURRENT APPLICATION NUMBER: US/09/747,287
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/08/802,981
PRIOR APPLICATION NUMBER: US/08/802,981
PRIOR PILING DATE: 1999-09-11
NUMBER OF SEQ ID NOS: 242
SOFTWARE: PACENTIN VERSION 3,2
SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
             APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: TUGHES, Richael
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEO ID NOS: 34
SOFTWARE: PATENTIN VENSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41.5; DB 9; Length 9;
Pred. No. 1.2e+06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (5).7(5)
OTHER INFORMATION: Xaa is norleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09747287
Publication No. US20030207264A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.18;
90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CISVPL-VPC 9
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-761-636A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-747-287-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-747-287-1
                                                                                                                                                                                                                                                                                                                            SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

RESULT 4 US-09-874-350A-1

```
Sequence 1, Application US/09814350A

publication No. US20001096926A1

GENERAL INFORMATION:

APPLICANT: Oncoimmunin, Inc.

APPLICANT: Romoriya, Akira

APPLICANT: Romoriya, Akira

APPLICANT: Reckard, Beverly

ITILE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S

ITILE OF INVENTION: AND METHODS OF USE THEREOF

FILE REFERENCE: 300-903840US

CURRENT FILING DATE: 2001-06-04

PRIOR FILING DATE: 2000-09-11

PRIOR FILING DATE: 1998-09-10

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1997-02-20

NUMBER OF SEQ ID NOS: 221

SOFTWARE: Patentin version 3.0

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USECULE 5

USECULATE 15

USECULATION NO. USCOUTOS 626A1

SEQUENCE 184, Application US/09874350A

SEPLICANT: Concoimmunin, Inc.

APPLICANT: Concoimmunin, Inc.

APPLICANT: Composition With Beverity

TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL STILLS OF INVENTION: AND METHODS OF USE THEREOF

TITLE OF INVENTION: AND METHODS OF USE THEREOF

TITLE OF INVENTION: AND METHODS OF USE THEREOF

TITLE OF INVENTION UNMBER: US/09/874,350A

CURRENT FILING DATE: 2001-06-04

PRIOR FILING DATE: 1998-02-20

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1999-09-10

PRIOR FILING DATE: 1999-09-10

NUMBER OF SEQ ID NOS: 221

SOFTWARE: PARENTEN VARIABE: 1997-02-20

NUMBER OF SEQ ID NOS: 221

SECOTION NO 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%; Score 33; DB 12; Length 9; 50.0%; Pred. No. 1.2e+06; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic peptide substrate NAMENT MAN (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) NAME (MAN ) N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (5)...(5)
; OTHER INFORMATION: Xaa is norleucine (Nle)
US-09-874-350A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: protease indicator NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (5)..(5)
OTHER INFORMATION: X is norleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| |:||
2 AIPXSIPC 9
```

Sun Sep

```
US-10-116-275-101

Sequence 101, Application US/10116275

Publication No. US20030211476A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1
SEQ ID NO 101
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                              CISVPLSVPC 10
                                                                 CLPVLLAAPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CLPVLLAAPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-116-275-101
                                                           g
                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                      ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                  Sequence 13, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinila, Clemencia
APPLICANT: Pinila, Clemencia
APPLICANT: Pinila, Clemencia
APPLICANT: Houghten, REChard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
CURRENT ELLE REFERENCE: 2002-10-15
CURRENT FILING DATE: 2002-10-15
SOFTWARE OF SEQ ID NOS: 119
SOFTWARE PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 71, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRABE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
TITLE OF INVENTION: MUMBER: US/10/126,845
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILING DATE: 2002-10-15
SOFTWARE: Patentin version 3.1
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 32; DB 14; Length 10; 50.0%; Pred. No. 1.3e+02; tive 2; Mismatches 3; Indels
                                             Length 9;
                                    58.9%; Score 33; DB 12; Length 9; 50.0%; Pred. No. 1.2e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Score 32; DB 14; Length 10; 50.0%; Pred. No. 1.3e+02; tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: membrane translocating peptide, cyclic US-10-126-845-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (1) ...(10)
; OTHER INFORMATION: D form amino acid
US-10-126-845-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: D form peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                Query Match 58.9
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CLPVLLAAPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE LOCATION: (1)...(10)
                                                                                                                   3 SVPLSVPC 10
                                                                                                                                         ::| |:||
2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
JS-09-874-350A-184
                                                                                                                                                                                                                                 US-10-126-845-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-126-845-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 13
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 71
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                   à
                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance UF OTHER INFORMATION: take Across the GIT"
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: Elan Pharmaceutical Technology
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Liea
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
CURRENT APPLICATION NUMBER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-10-764-235-13
US-10-764-235-13
Sequence 13, Application US/10764235
Publication No. US20040138132A1
GENREAL INFORMATION:
APPLICANT: O'MAHONY, Daniel J.
APPLICANT: Lambkin, Imelda J.
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFREENCE, P26, 479-B USA
CURRENT APPLICATION NUMBER: USA
CURRENT PILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 09/671,089
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/156,246
PRIOR PILING DATE: 1999-09-27
PRIOR PILING DATE: 1999-09-27
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 3:
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: membrane translocating peptide, cyclic US-10-764-235-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 15;
Pred. No. 1.3e+02;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%; Score 32; DB 16;
50.0%; Pred. No. 1.3e+02;
tive 2; Mismatches 3;
```

염

```
US-09-932-165-794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                      dd
                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                   APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARITANO, ARTHUR
APPLICANT: FRAIS, MARY
APPLICANT: AFAR, DOUGLAS
APPLICANT: AFAR, DOUGLAS
APPLICANT: BEVIN, ELANA
APPLICANT: LEVIN, ELANA
APPLICANT: HUBERT, REN
APPLICANT: GE, WANGWAO
APPLICANT: GI, WANGWAO
APPLICANT: BISPLIA
APPLICATION: NUGLEIC AID
ATTLE OF INVENTION: BIPTION OF CANCER
TITLE OF INVENTION: BIPTION OF CANCER
TITLE OF INVENTION: WOMBER: US/09/932,165
CURRENT APPLICATION NUMBER: 60/226,329
PRIOR FILLING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SSOFTARE: PALENTIN VEY: 2.1
SEQ ID NO 284
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JAKOBOUTS, ANAMATANA AVA
APPLICANT: JAKOBOUTS, AVA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: B3P2H3 AND CATFFZEII USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REFERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2000-08-17
RIGH APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 184
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31.5; DB 10;
Pred. No. 1.2e+06;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 184, Application US/09932165
Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
                                                                                                      Sequence 284, Application US/09932165 Publication No. US20030134784A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHALLITA EID, PIA M.
FARIS, MARY
SAFRAN, DOUGLAS
AFAR, DANIEL
LEVIN, ELANA
HUBERT, RENE
GE, WANGMAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:: ||| ||
1 CLT-PLSFPC 9
1 CLPVLLAAPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-932-165-184
                                                                                      US-09-932-165-284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Websur: 12
US-09-932-165-560

US-09-932-165-560

Sequence 560, Application US/09932165

Publication No. US20301347841

APPLICANT: RAITANO. ARTHUR

APPLICANT: CHALLITA-EID, PIA M.

APPLICANT: FARIS, WARY

APPLICANT: AFRA, DANIEL

APPLICANT: BAFRAN, DOUGLAS

APPLICANT: LEVIN, ELANA

APPLICANT: HUBERT, RENE

APPLICANT: AFRAN, DANIEL

APPLICANT: HUBERT, RENE

TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

TITLE OF INVENTION: BAPLAIS AND

TITLE OF INVENTION: BAPLAIS

TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: SAFFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: HUBBRT. RENE
APPLICANT: JAKOBOVITS, ANA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: B3P2H3 AND CATFF2E11 USEFUL IN TREATMENT AND
TITLE OF INVENTION: DETECTION OF CANCER
FILE REPRENCES: 51156-22014.00
CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif US-09-932-165-560
, OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 10;
                                                                                                                                               Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.2%; Score 31.5; DB 10; 60.0%; Pred. No. 1.6e+02;
                                                                                                                                           Score 31.5; DB 10;
Pred. No. 1.6e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 794, Application US/09932165 Publication No. US20030134784A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                   Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                               1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CLT-PLSFPC 9
                                                                                                                                                                                                                                                                                                                                                                    |:: ||| ||
1 CLT-PLSFPC 9
```

1;

```
Search completed: September 5, 2004, 11:40:12 Job time : 67 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-363-791-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PLSAPC
                                                                              US-10-363-791-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US 10186,126
PRIOR PELICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/180,479
PRIOR PILING DATE: 2000-03-17
PRIOR PELING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ή;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif US-09-932-165-794
                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                              56.2%; Score 31.5; DB 10; Length 10; 60.0%; Pred. No. 1.6e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.4%; Score 31; DB 15; Length 9; 71.4%; Pred. No. 1.2e+06; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1121, Application US/10154884B
Publication No: US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 794
LENGTH: 10
                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |:: || || CLT-PLSFPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-154-884B-11221
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CISVPLS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-10-154-884B-11221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

|:|||:| 2 CLSVPVS 8

```
0
                                                                 APPLICANT: TAKINGTO, Masato
APPLICANT: TAKINGTO, Masato
APPLICANT: TAKINGTO, Masato
APPLICANT: TAKINGTO, No. US20040029197Aloru
APPLICANT: SATO, No. US20040029197Aliyuki
APPLICANT: SAFARA, Hiroeki
ITILE OF INVENTION: A novel human cancer/testis-associated gene thereof
FILE REFERENCE: 44394006
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US 2000-274218
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn version 3.2
SEQ ID NO 194
LENGTH: 10
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.4%; Score 31; DB 12; Length 10; 83.3%; Pred. No. 1.9e+02; tive 0; Mismatches 1; Indels
Sequence 194, Application US/10363791
Publication No. US20040029197A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.4
Best Local Similarity 83.3
Matches 5; Conservative
```

**This Page** Blank (uspto)

```
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 4; Conserv
   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                  94105
                                                                                                                                                                                                                                             US-08-331-383-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-331-383-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43, Appl
Sequence 143, Appl
Sequence 142, Appl
Sequence 142, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appli
Sequence 30, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Appl Sequence 10, Appl Sequence 1, Appli Sequence 5, Appli Sequence 17, Appli Sequence 17, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 147, App
Sequence 148, App
Sequence 149, App
Sequence 150, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 33, Appl
Sequence 43, Appl
                                                         5, 2004, 11:32:18; Search time 15 Seconds (without alignments) 34.417 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                     /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                            389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                               Issued Patents AA:*
                                                                                                    US-09-761-636A-13
56
1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                            September
                                                                                                                                                                                                                   Minimum DB seq length: 0 Maximum DB seq length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein
                                                                                                                                                                                                                                                                                             Database :
                                                                                                                         Sequence:
                                                                                                                                                                            Searched:
                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Result
No.
```

```
Sequence 33, Application US/08331383

Sequence 33, Application US/08331383

Fatent No. 5605809

GENERAL INFORMATION:
APPLICANT: Romoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                        371, Apr

(Applied of Applied of 
                                                                                                                               Sequence 3
                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
Sequence
                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-OCT-1994
CLLASSIFPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B:
REGISTRATION NUMBER: 29,684
REGISTRATION NUMBER: 29,684
                      US-08-471-068-148
US-08-471-068-149
US-08-471-068-149
US-08-11-784A-371
US-09-187-330-6
US-09-187-330-28
US-09-187-330-28
US-09-187-330-28
US-09-187-330-33
US-09-187-330-33
US-09-187-330-33
US-09-187-330-33
US-09-187-330-33
US-08-891-271-4
US-08-931-402-13
US-08-931-402-13
US-08-933-402-13
US-08-933-402-13
US-08-933-402-13
US-08-933-402-13
US-08-933-402-13
US-08-933-402-13
US-08-933-402-13
US-08-933-402-13
US-08-931-918-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1686
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELERAX: 415-326-242
INPORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
```

0;

Gaps

.;

64.3%; Score 36; DB 1; Length 9; 50.0%; Pred. No. 3e+05;

4; Mismatches

```
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-331-383-31
; Sequence 31, Application US/08331383
; Patent No. 5605809
; CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-802-981-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|:|:|
2 AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
US-08-544-008 43
US-08-544-008 43
US-08-544-008 43
US-08-544-008 43

PACENT NO. 5711342

GENERAL INFORMATION:

APPLICANT: Packard, Beverly S.

TITLE OF INVENTION: Compositions for the Detection of TITLE OF INVENTION: Procease in Biological Samples and Methods of Use Thereof NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

STREET: Two Embarcadero Center, Eighth Floor

STATE: California

CONDUTER: Law Compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 143, Application US/08802981
; Sequence 143, Application US/08802981
; Patent No. 6037130:
; GENERAL INFORMATION:
APPLICANT: Romoriya, Akira
APPLICANT: Reackard, Bevealty S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
SIRRET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 9;
Pred. No. 3e+05;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 9 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-549-008-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::|:|:|
2 AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

```
APPLICANT: Romoriya, Akira
APPLICANT: Romoriya, Akira
APPLICANT: Romoriya, Beverly S.
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 38,498
REFERENCE/COCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids

LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-OCT-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 3;
Pred. No. 3e+05;
```

ö

TOPOLOGY: linear

g

```
Sequence 142, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Remoriya, Akira
APPLICANT: Remoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
FORRESPONDENCE: 231
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08212190A
Patent No. 565223
GENERAL INFORMATION:
APPLICANT: KOHN, Elise C.
APPLICANT: KIM, Young Sook
TITLE OF INVENTION: UNA ENCODING CAI RESISTANCE PROTEINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.9%; Score 33; DB 3; Length 9; 50.0%; Pred. No. 3e+05; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          COMPUTER: USA

ZIP: 9411-3834

ZIP: 9411-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMER: 20-FEB31997

FILING BATE: 20-FEB31997

--ANTION: --ANTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                016865-000300US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 5
OTHER INFORMATION: /product= "Nle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HULTER, TOM
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 01686
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site LOCATION: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.9
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                       JS-08-802-981-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-802-981-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-212-190A-5
                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Komoriya, Akira
APPLICANT: Komoriya, Akira
APPLICANT: Romoriya, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: The Differnia
                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                       Score 33; DB 1; Length 9;
Pred. No. 3e+05;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: JUSA
ZIP: 9411-3834
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-OCT 1995
FILING PAPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/331,383
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 32,762
RELECOMMULICATION INFORMATION:
TELERHONE: (415) 576-0200
                                         NAME/KEY: Region
LOCATION: one-of(5)
COTHER INFORMATION: /note= "Xaa is norleucine.
US-08-331-383-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 1;
Pred. No. 3e+05;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /product= "Nle"
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42, Application US/08549008
Patent No. 5714342
GENERAL INFORMATION:
                                                                                                                                                     Query Match 58.9%;
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 amino acids
MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                          3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SVPLSVPC 10
                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                          US-08-549-008-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-549-008-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
```

ò

```
PCT-US95-03610-5; Sequence 5, Application PC/TUS9503610; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-461-697-21
; Sequence 21, Application US/09461697
sequence 21, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
                                                                                                                                                                                                                                   44.68;
TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: E SEQUENCE CHARACTERISTICS:
                                                                 LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.4'
                                                                                                                                                                                                                                                      Local Similarity 66.7
ses 4; Conservative
                                                                                                                                         TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-900-321-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CVMTHLSLP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CISVPLSVP 9
                                                                                                                                                                                                                                                                                                                             5 PLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                           3 PAPVPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-461-697-21
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ob
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08900321

Patent No. 5981712

Patent No. 5981712

APPLICANT: Kohn, Elise C.

APPLICANT: Liotta, Lance A.

APPLICANT: Kim, Young S.

APPLICANT: Kim, Young S.

TITLE OF INVENTION: Uses Thereof

NUMBER OF SEQUENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

CORRESPONDENCES: 10

COUNTRY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PatentIn Release #1.0, Version #1.30

CORRESTION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #10, Version #1.30

CURRENT APPLICATION NUMBER: US/08/900,321

FILING DATE: 25-JUL-1997

CLASSIFICATION NUMBER: US 08/212,190

FILING DATE: 14-MAR-1994

ATORNEY AGENT INFORMATION:

ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 15280-204US
REFERENCE/DOCKET NUMBER: 15280-204US
REFERENCE/DOCKET NUMBER: 15280-204US
REPERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-560
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.6%; Score 25; DB 1; Length 10; 66.7%; Pred. No. 2.7e+02; tive 0; Mismatches 2; Indels
                        ZIP: 94105-1493

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATCHIL Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hunter, Tom REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-204100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PAPVPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-212-190A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-900-321-5
         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
publicant incornation:

APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Thomas, Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: Puranam, Kasturi
APPLICANT: ANENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILLE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 10
                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                    Gaps
                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA ENCODING CAI RESISTANCE PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.6%; Score 25; DB 3; Length 10;
44.4%; Pred. No. 2.7e+02;
tive 2; Mismatches 3; Indels
      Length 10;
                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.25
Score 25; DB 2; 1
Pred. No. 2.7e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: DNA ENCODING CAI RE
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PETOPPY disk
COMPUTER: PETOPPY disk
COMPUTER: PETOPN MAS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03610
FILING DATE: 14-MAR-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
```

ö

```
GENERAL INCRMATION:

GENERAL INCRMATION:

APPLICANT: HAMILTON, BRUCE K.

APPLICANT: TUGSTNEXT, GEORGE P.

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 07266-000

CURRENT PILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 07/483,527

PRIOR APPLICATION NUMBER: 07/483,527

PRIOR FILING DATE: 1995-05-22

PRIOR FILING DATE: 1995-05-22

PRIOR FILING DATE: 1995-05-22

PRIOR FILING DATE: 1995-01-24

PRIOR FILING DATE: 1995-03-22

PRIOR FILING DATE: 1995-03-36

PRIOR SELING DATE: 1995-03-36

PRIOR PLING DATE: 1995-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: analog of thrombospondin US-08-476-134A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
42.9%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.9%; Score 24; DB 3; Length 6; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; APPLICANT: EYAL, JACOB, HAMILTON, BRUCE K., TUSZYNASKI, ;GEORGE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/08476134A Patent No. 6239110 GENERAL INFORMATION:
                                               TELEPHONE: (215) 567-2020
TELEFAX: (215) 567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                           TELECOMMUNICATION INFORMATION
                                                                                                                                                             21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.9
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SVPC S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SVPC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
5190920-26
;Patent No. 5190920
                                                                                                                                                                                                                                                                                                                                                                                           US-08-483-434A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-476-134A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/08483434A
Patent No. 5648461
GENERAL INFORMATION:
APPLICANT: EVAL, Jacob
APPLICANT: HAMILTON, Bruce K.
APPLICANT: TUSZYNSKI, George P.
TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
TITLE OF INVENTION: Therapeutic Use Thereof
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 5; Length 10;
Pred. No. 2.7e+02;
0; Mismatches 2; Indels
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Webber, Kennech 3, 6,7
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9603
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: PANITCH SCHWARZE JACOBS & NADEL, P.C. 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,434A FILIG DATE: CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-3U6 (9049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA

APPLICATION DATA:
APPLICATION NUMBER: US 08/450,738
FILING DATE: 25-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/185,614
FILING DATE: 24-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,436
FILING DATE: 01-MAR-1993
PRIOR APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
PRIOR APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
PRIOR APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
PRIOR APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
FRIOR APPLICATION NUMBER: US 07/483,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 44.6%;
Best Local Similarity 66.7%;
Matches 4; Conservative (
                                                                                                                                                                                                                                                                                                                                                                             10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 PLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PAPVPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-483-434A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-03610-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                LENGIH:
```

à

ò

```
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35. Application US/08331383
| Patent No. 5605809 |
| Patent No. 5605809 |
| GENERAL INFORMATION: Akira |
| APPLICANT: Komoriya, Akira |
| APPLICANT: Packard, Beverly S. |
| TITLE OF INVENTION: Compositions for the Detection of TITLE OF INVENTION: Thereof |
| TITLE OF INVENTION: Thereof |
| VUMBER OF SEQUENCES: 56 |
| CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew |
| STREET: One Market Plaza, Steuart Tower, Suite 2000 |
| CITY: San Francisco |
| STABET: California |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: NO. 1005 |
| CONTENTION: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
THROMBOSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
NUMBER OF SEQUENCES: 45
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,181
FILING DATE: 22-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 131,565
FILING DATE: 04-OCT-1993
APPLICATION NUMBER: 895,764
FILING DATE: 09-JUN-1992
APPLICATION NUMBER: 895,764
FILING DATE: 09-JUN-1992
APPLICATION NUMBER: 895,764
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                     42.9%; Score 24; DB 6; Length 6; 100.0%; Pred. No. 3e+05; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/331,383
FILING DATE: 28-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.9%; Score 24; DB 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,197
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                         Query Match 42.9
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SVPC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVPC 5
                                                                                                                                                           LENGTH: 6
5190920-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-331-383-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;SEQ ID NO:28:
                                                                                                                              SEQ ID NO:26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5506208-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEORGE P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region

: LOCATION: one-of(8)

: OTHER INFORMATION: /note= "Xaa is Pro or aminoisobutyric

: OTHER INFORMATION: acid."

US-08-331-383-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.9%; Score 24; DB 1; Length 9; 37.5%; Pred. No. 3e+05; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                               /note= "Xaa is Met or norleucine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: September 5, 2004, 11:35:35 Job time : 16 secs
                                                                                 16865-1
             ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGIENATION UNMERE: 29,684
REFERENCE/DOCKET NUMBER: 1686:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 37.5
Matches 3; Conservative
                                                                                                                                                                                                          LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Region
LOCATION: one-of(5)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AIPXSIXC 9
CLASSIFICATION:
```

0

```
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
```

OM protein - protein search, using sw model

5, 2004, 11:00:28; Search time 11.667 Seconds (without alignments) 74.205 Million cell updates/sec September Run on:

US-09-761-636A-14 52 1 CISVPLVPC 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

790 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 4 0 E 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	546 MHC H2-L antiden	glycogen	118K ston	locus		) tetrameric pr			qlyco			180 60K Ca binding pro			ATPase	T-cell re	flagel	ro	endoglyco		conopr		Ig heavy	collagen alpha	R-phycoerythrin		alpha-1 4-c1uca	
		I655	0	A60356	A61620	S1078	S66419	I51049	\$13636	H48394	G33098	I54017	PTOO	148105	82128	D48186	PH0943	E42364	842620	B39745	A42689	B28495	PT0247	PT0268	\$26508	B22565	B34835	B26206	
	DB	i ! (2)	~	N	7	7	7	C)	~	N	~	4	~	N	~	7	7	7	7	7	7	7	7	7	7	7	7	~	
	Length	9	Ŋ	6	σ	60	6	4	σ	Q	80	<b>0</b> 0	σ	7	æ	σı	9	Ŋ	7	80	80	σ	σ	6	σ	5	49	φ	
de	ery	1 8	9	36.5	4.	32.7	32.7		٥.	28.8	8	œ	œ	26.9	ė	26.9	9	S	S	25.0	25.0	S	S	25.0	5	ω.	23.1	e,	
	Score	22	19	19	18	17	17	16	16	15	15	15	15	14	14	14	14	13	13	13	13	13	13	13	13	12	12	12	
	Result No.		7	æ	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	

seed protein ws-5	T-cell receptor be	hypothetical prote	neutral proteinase	T-cell receptor be	sperm-activating p	kidney and bladder	phosphoenolpyruvat	3',5'-cyclic-GMP p	T-cell receptor be	T-cell receptor be	T-cell receptor be	T-cell receptor be	T-cell receptor be	
E61491	PH0932	S16324	A35180	PH0934	S19329	G58502	355696	A53797	PH0935	PH0937	PH0902	PH0917	PH0918	PH0921
0,0	4 (1	7	N	~	(7	~	N	7	Ŋ	N	۲3	~	7	73
7		8	80	80	6	6	6	δ	6	6	6	σ,	σ	9
23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1
12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
30	35	33	34	32	36	3.7	38	39	40	41	42	43	44	45

## ALIGNMENTS

Ø	ences		0 ;
v-199	nbəs ə	1234	0; Gaps
05-Nc	r-like	D:9554	0;
change	nhance	.1; PI	h 6; dels
#text_	ter: E 0743	A39663	Lengt ; 0; In
-1996	sky, P promo ID:351	L/DDBJ IDN:AA	DB 2; .8e+05 es
02-Aug	Kourıl H-2Kb 02; PM	3B/EMB 565; P	22; No. 2 smatch
t) use) ision	, O.; mouse 861062	from D:g199	Score 22; DB 2; Length 6; Pred. No. 2.8e+05; 1; Mismatches 0; Indels
RESULT 1 165546 MHC H2-L antigen - mouse (fragment) MHC H2-L antigen - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999 C;Accession: 165546	Kiximura, A.; Israel, A.; Le Ball, O.; Kourilsky, P. Cell 44, 261-272, 1986 A.Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences A;Reference number: 152778; MUID:86106202; PMID:3510743 A;Accession: 165546	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-6 <res> A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234</res>	
use (fus (fos (fos (fos (fos (fos (fos (fos (fo	A.; L	; tran	y 7 ervati
n - mou musculu 1996 #3	srael, 2, 1986 ed ana oer: 19	ninary : DNA <res></res>	nilarit Conse
antiger Musr 2-Aug-1	A.; 18 261-27 26taile 3e num 3e num 3n: 169	preline type:	itch al Sir 3;
RESULT 1 165546 MHC H2-L antigen - m C.Species: Mus muscu C, Date: 02-Aug-1996 C, Accession: 165546	kikimura, A.; Israel, V Cell 44, 261-272, 1986 A;Title: Detailed anal) A;Reference number: 15; A;Accession: 165546	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-6 <res> A;Cross-references: G</res>	Query Match Best Local Similarity 75.0%; Matches 3; Conservative
RESULT 165546 MHC H2. C;Spec C;Date C;Acces	K; Ki Cell A; Ti A; Re	A; St A; Mc A; Re A; Cr	QWE

and thei

: | | | MVPC 4 6 LVPC 9 8 g

Accession: A60521
Ascession: A

Query Match
36.5%; Score 19; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels

ö

Gaps

.,

2 ISVP 5 2 ISVP d à

```
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S66419
R;Kuwabara, T.
REBS Lett. 371, 195-198, 1995
A;Title: The 60-KDa precursor to the dithiothreitol-sensitive tetrameric protease of spinA;A;Reference number: S66419; MUID:95402209; PMID:7672127
A;Accession: S66419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metallothionein-A - rainbow trout (fragment)
C;Species: Oncortynchus myKiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Brolsen, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus myKiss) meA;Reference number: 151049; MUID:95324545; PMID:7601121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coat protein beta chain, Golgi-derived - rabbit (fragment)
N.Alternate names: beta-COP protein
C,Species: Oryctolagus cuniculus (domestic rabbit)
C,Species: Oryctolagus cuniculus (domestic rabbit)
C,Accession: 813636
R,Serafini, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orci, L.; Rothman, J.E.; Wiels Nature 349, 215-220, 1991
A,Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to the A,Reference number: 813636, WUID:91101693; PMID:1898984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PID:94379328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

30.8%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.8%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                32.7%; Score 17; DB 2; Length 9; 50.0%; Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: 151049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Refidues: 1-9 <SER:
Superfamily: coatomer complex beta chain
C;Keywords: Golgi apparatus; protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 1-9 < KUW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::|
PILP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-4 <OLS>
                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 VPLV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IPIV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 PC
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 813636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                           Int. J. Cancer 45, 783-787, 1990
A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A;Reference number: A60356; MUID:90216080; PMID:2323853
A;Accession: A60356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A. Insect Biochem. Mol. Biol. 22, 447-452, 1992
A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add A;Reference number: A61620
A;Accession: A61620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S10783
R;Strawich, E.; Glimcher, M.J.
R;Strawich, E.; Glimcher, M.J.
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                      ö
                     C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60356
R;Shiraishi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     locustamyotropin III - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C;Accession: A61620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enamelin f - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Status: preliminary
A,Molecule type: protein
A,Roblecule type: protein
C,Residues: 1-9 <SCH>
C,Reywords: amidated carboxyl end; neuropeptide
P,9/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34.6%; Score 18; DB 2; Length 9; 75.0%; Pred. No. 2.8e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.7%; Score 17; DB 2; Length 8; llarity 60.0%; Pred. No. 2.8e+05; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                Score 19; DB 2; I
Pred. No. 2.8e+05;
1; Mismatches 1;
118K stomach cancer antigen - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: protein
A,Residues: 1-8 <STR>
C,Keywords: enamel; phosphoprotein
                                                                                                                                                                                                                                                                                                                                   36.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75,000
Best Local 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-9 <SHI>
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|| |
1 IPLKP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 PFVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
```

m

ô

RESULT 9

```
C;Species: Rana esculenta (edible frog)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: Pr0080
R;Treveso, S.; Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.
Biochem. Biochora. Res. Commun. 175, 444-450, 1991
A;Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calret: A;Reference number: PT0080; MUID:91207333; PMID:2018493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Nuclectide sequence and nuclease hypersensitivity of the Chinese hamster dihydr A,Reference number: 148105, MUID:87076541, PMID:3024702 A,Accession: 148105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Solarum tuberroum (potato)
C;Species: Solarum tuberroum (potato)
C;Accession: S21288
C;Accession: S21288
R;Millar, D.G; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P.
Biochem. J. 283, 813-821, 1992
Biochem. J. 283, Bill-Binding proteins in potato (Solarum tuberosum L.) tuber. Characterizatio A;Accession: S21288; WUID:9222683; PMID:1590771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dihydrofolate reductase - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Bate: 04-85p-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Accession: I48105
R;Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
Biochemistry, 25, 6228-6236, 1986
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: M14771; NID: g191055; PIDN: AAA36975.1; PID: g191056
     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-8 <ML>
A;Residues: 1-8 <ML>
C;Experimental source: var. Ulster Sceptre
C;Function:
A;Description: may be involved in defence mechanism of the plant
C;Keywords: hydroxyproline; lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14; DB 2; Length 7;
Pred, No. 2.8e+05;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
     ..
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 28.8%; Score 15; DB 2; Le Similarity 100.0%; Pred. No. 2.8e+05; 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-7 <RES>
     Mismatches
                                                                                                                                                                                                                               60K Ca binding protein - edible frog (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lectin - potato (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <TRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                    9
                                                   PLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:
4 PLI 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: PT0080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PLV 7
                                                                                                    PLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PLV 7
3;
                                                   S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                         g
                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                              glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: H48394 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Riochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: human gene engineered and expressed in Echerichia coli
C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C;Accession: 154017
R;Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.
Gene 65, 13-22, 1988
A;Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
G33098
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falcipārum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: G33098
R;Nichols, J.H.; Hager, L.P.
Submitted to the Protein Sequence Database, May 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-8 <DEV>
A;Cross-references: GB:M20922; NID:g806638; PIDN:AAA66353.1; PID:g183043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    granulocyte-colony stimulating factor precursor - synthetic (fragment)
C,Species: synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.8%; Score 15; DB 2; Length 6; 50.0%; Pred. No. 2.8e+05; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: sequence extracted from NCBI backbone (NCBIP:131518) C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                     II-like sequences.
A.Reference number: A48394; MUID:93250576; PMID:8485470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: 154017; MUID:88284374; PMID:2456256
A;Accession: 154017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%; Score 15; DB 2; Le
100.0%; Pred. No. 2.8e+05;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.8%; Score 15; DB 4; 375.0%; Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-6 <MAT>
A,Experimental source: milk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: A33098
A;Accession: G33098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-8 <NIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 VPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VELLGC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Status: preliminary
                                                                                                                                                                                                                                                                                                                           A; Accession: H48394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPL 4
```

0

ð ద

o ,

à g

```
Arease RI subunit - wood tobacco (fragment)
C,Species: Nicotiana sylvestris (wood tobacco)
C,Species: Nicotiana sylvestris (wood tobacco)
C,Accession: D48186
R;De Peape, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A;Title: Specific mitcohondrial proteins in pollen: presence of an additional ATP syntha
A,Reference number: A48186; MUID: 93317598; PMID: 8327463
A,Molecule type: protein
A,Molecule type: protein
A,Residues: 1-9 < DEI>
A,Residues: 1-9 < DEI>
A,Residues: 1-9 < CDEI>
A,Residues: 1-9 < CDEI>
A,Rote: sequence extracted from NCBI backbone (NCBIP:134871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 26.9%; Score 14; DB 2; Length 9; Best Local Similarity 60.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 2; Indels
Query Match
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 3; Indels
                                                                                                               3 SVPLVP 8
                                                                                                                                                                  3 STPSPP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VDLAP 7
                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                 ò
```

Search completed: September 5, 2004, 11:06:22 Job time : 11.6667 secs

```
conus purpu
locusta mig
homo sapien
periplaneta
homo sapien
litoria rub
conus stria
mytilus edu
cydia pomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusarium so
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stomopneute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             herpes simp
enterococcu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thunnus obe
locusta mig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ascaris suu
squalus aca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   penaeus mon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treponema h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bufo regula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leptinotars
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pachymedusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         herpes simp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     litoria rub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     periplaneta
pichia jadi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P29177 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            5, 2004, 10:57:02; Search time 7 Seconds (without alignments) 66.947 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P30089
P82692
P302618
P302096
P05487
P05487
P05487
P30087
3008
P3008
P3008
P3008
P3008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P42984
P81455
P81780
P81780
P16339
P42999
P32878
P82926
P829265
P82065
P82065
P82065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P41489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141681 seqs, 52070155 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COW2_CONPU
LMT3_LOCMI
UPA3_LOCMI
UPA3_LOCMI
UPA3_PERAM
PPK2_PERAM
UPA7_PERAM
HI01_LITRU
COND_CONST
COND_CONST
COND_CONST
COND_CONST
COND_CONST
COND_CONST
CONST
CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAR9 ASCSU
OXYA SQUAC
OXYT RABIT
RT33 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COW CONVE
PPK1 PERAM
TAL1 PICJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Π
                                                                                                                                                                                                                                                                         US-09-761-636A-14
52
1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SwissProt_42:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                               September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
No.
```

19.2   1	adi rub rub edu edu edu per nas fu fu fu fu fu							·. 0	
14 10 19.2 9 1 TAL3 FICUA  36 9 17.3 5 1 E103_LITRU  39 9 17.3 6 1 CIPL_MYTED  40 9 17.3 6 1 CIPL_MYTED  41 9 17.3 6 1 CIPL_MYTED  42 9 17.3 7 1 BRHP_CONIM  43 9 17.3 7 1 WMA2_ACHFU  44 9 17.3 7 1 WMA2_ACHFU  44 9 17.3 7 1 WMA2_ACHFU  45 9 17.3 7 1 WMA2_ACHFU  46 9 17.3 7 1 WMA2_ACHFU  47 9 17.3 7 1 WMA2_ACHFU  48 9 17.3 7 1 WMA2_ACHFU  49 17.3 7 1 WMA2_ACHFU  40 17.3 7 1 WMA2_ACHFU  41 9 17.3 7 1 WMA2_ACHFU  42 9 17.3 7 1 WMA2_ACHFU  43 9 17.3 7 1 WMA2_ACHFU  44 9 17.3 7 1 WMA2_ACHFU  45 9 17.3 7 1 WMA2_ACHFU  46 9 17.3 7 1 WMA2_ACHFU  47 9 17.3 7 1 WMA2_ACHFU  48 9 17.3 7 1 WMA2_ACHFU  48 9 17.3 7 1 WMA2_ACHFU  49 17.3 7 1 WMA2_ACHFU  40 17.3 7 1 WMA2_ACHFU  41 9 17.3 7 1 WMA2_ACHFU  42 9 17.3 8 1 ACT_CRAEG  41 0 17.3 7 1 WMA2_ACHFU  42 0 17.3 7 1 WMA2_ACHFU  43 0 17.3 7 1 WMA2_ACHFU  44 9 17.3 7 1 WMA2_ACHFU  45 0 17.3 7 1 WMA2_ACHFU  46 17.3 7 1 WMA2_ACHFU  47 0 17.3 8 1 ACT_CRAEG  48 0 17.3 8 1 ACT_CRAEG  48 0 17.3 8 1 ACT_CRAEG  48 0 17.3 7 1 WMA2_ACHFU  48 0 17.3 8 1 ACT_CRAEG  5 0 17 CCT_CONEU	pichia j litoria mitilus mytilus conus im conus pi pinus pi achatina achatina achatina carcinus			1.63) (6		nnine-DNA cometrically systeine enzyme is	+ protein RANSFERASE	10	
14 10 19.2 9 1 TAL3 FICJA  36 9 17.3 5 1 EIO3_LITRU  39 9 17.3 6 1 CIPL_MYTED  39 9 17.3 6 1 CIPL_MYTED  40 9 17.3 6 1 CIPL_MYTED  41 9 17.3 7 1 UNO6_PINPS  42 9 17.3 7 1 UNO6_PINPS  43 9 17.3 7 1 UNO6_PINPS  44 9 17.3 7 1 UNO6_PINPS  45 9 17.3 7 1 UNO6_PINPS  46 9 17.3 7 1 UNO6_PINPS  47 1 0 17.3 7 1 UNO6_PINPS  48 1 ACT_GARHTU  49 17.3 7 1 UNO6_PINPS  49 17.3 7 1 UNO6_PINPS  49 17.3 7 1 UNO6_PINPS  40 17.3 7 1 UNO6_PINPS  41 9 17.3 7 1 UNO6_PINPS  42 17.3 8 1 ACT_GARHTU  43 9 17.3 7 1 UNO6_PINPS  44 9 17.3 7 1 UNO6_PINPS  45 17.3 8 1 ACT_GARHTU  46 9 17.3 7 1 UNO6_PINPS  47 1 UNO6_PINPS  48 1 ACT_GARHTU  49 17.3 7 1 UNO6_PINPS  49 17.3 7 1 UNO6_PINPS  49 17.3 8 1 ACT_GARHTU  40 17.3 7 1 UNO6_PINPS  41 1 ACT_CAGATON  42 17.3 8 1 ACT_GARHTU  43 17.3 8 1 ACT_GARHTU  44 9 17.3 7 1 UNO6_PINPS  45 17.3 8 1 ACT_GARHTU  46 17.3 7 1 UNO6_PINPS  47 1	P1174 P820 P820 P821 P3317 P359 P359 P359 P359			(EC 2.1	; Eutel	. O6-methylgua NA by stoichi sition to a c	thylguanine) thylguanine) iD OGT METHYLJ iS. TOR (BY SIMII	Length 9 ; 1; Indel	
34 10 19.2 9 1 TAL3 FIG 35 9 17.3 5 1 E103_L17 38 9 17.3 6 1 CIP1_MYT 38 9 17.3 6 1 CIP1_MYT 39 9 17.3 6 1 CIP2_MYT 40 9 17.3 7 1 UNO6_FOR 41 9 17.3 7 1 UNO6_FOR 42 9 17.3 7 1 WWA3_ACI 43 9 17.3 7 1 WWA3_ACI 44 9 17.3 7 1 WWA3_ACI 44 9 17.3 7 1 WWA3_ACI 45 9 17.3 7 1 WWA3_CACI 46 9 17.3 7 1 WWA3_CACI 47 9 17.3 7 1 WWA3_CACI 48 9 17.3 7 1 WWA3_CACI 49 17.3 7 1 WWA3_CACI 49 17.3 7 1 WWA3_CACI 49 17.3 7 1 WWA3_CACI 40 17.3 7 1 WWA3_CACI 41 9 17.3 8 1 ACT_CARP 42 9 17.3 7 1 WWA3_CACI 43 9 17.3 8 1 ACT_CARP 44 9 17.3 7 1 WWA3_CACI 40 10-DEC-1992 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CT-1996 (Rel. 24, Last sequence 61-0CNPU 61-0CT-1992 (Rel. 24, Last sequence 61-0CNPU 61-0CM-10CT-1992 (Rel. 24, Last sequence 61-0CNPU 61-0CNPU 61-0CNPU 61-0CM-10CM-10CNPU 61-0CNPU 61-0C	«DDQQE«DDD	ENTS	9 AA.	pdate) update) yltransfe (Fragment	a; Verteb Ruminanti	ne bovine nine in D ne O-6 po suicide r	ut 6-0-me il ADA AN RESIDUE srase. UP ACCEP	1; e+05	8 AA. odate) update)
$\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega$	AL3_PICJ 103_LITR 104_LITR 1P1_MYTE 1P2_MYTE NPP_CONI NO6_PINP WA1_ACHF WA3_ACHF WA3_ACHF WA3_ACHF	ALIGNM	PRT;	) quence up notation ine methy ferase)	Craniata actyla, I	a tg	or E.COI OF E.COI OF E.COI ACCEPTOR AL. AL. AL. ALKYL GRC	Score 20; Pred. No. Mismat	
$\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega$				eated st sec st an cyste trans	data; rtiod	=23086 ran P sequent -21(19 -21) yl greent	MENTS ALKYL PARTII METRY ALKYL AJ 1 1 2 2 3 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		
$\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega$	0 N N O O O C C C C C C C C C C C C C C C		ANDARD;	24, Cr 24, La 34, La rotein- methyl	e). a; Chor a; Ceta Bos.	PubMed J., Kar o acid ."; .18:17 air of the alk e enzym	ysteine. ysteine. ITH SEG SS THE 97; Met MGMT; Ferase; 9	3 7 7ati	ANDARD; 41, Creat 41, Last 41, Last
$\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega_{\omega$	9777777777		ST	(Rel. (Rel. (Rel. DNAp	(Bovin Metazo utheri vinae;	us; 74912; Hall e amin ferase ds Res N: Repi rring ring	IC ACT II - L - CY II Y: W NCOMPA NCOMPA PR0014; Trans 1 9 9 AA;	ilarity Conse: PC 9	(Re (Re
$\omega_{i}\omega_{i}\omega_{i}\omega_{i}\omega_{i}\omega_{i}\omega_{i}\omega_{i}$	0		IN F BOVIN	177; DEC-1992 DEC-1992 DCT-1996 Tylated-	itaurus ryota; alia; E dae; Bc TaxID=	JENCE. SUE=Thymical Subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence of the subsequence	CATALYT [protein S-methy S-methy SIMILAR WHICH BY WHICH BY BERFO; I STER SITE SITE SITE SITE SITE SITE SITE SITE	atc] cal	2 NNPU 58785; 8-FEB-2003 8-FEB-2003
SOLITE DO SOLITE MARKEN SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SOLITE DE SO	66666664444444444600000000000000000000		SULT 1	001-1-0001-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	Bos Bos Mamr Bov	LIJ SEQU TISK TISK MEDI RYGH "ACCH MCJ	-!- Inte PROS DNA NON NON SEQT	wery Nest Lo	F S S F S S S
			MG.	888888	800000	R R R R R R R R R R R R R R R R R R R	SO THE TAKE BY	A W B B B B B B B B B B B B B B B B B B	RES COW ID AC DT DT

```
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                        NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLEP 5
                                                                                                                                                                                                  TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPK2_PERAM
TD__PPK2_PERAM
                                  UPA3 HUMAN P30089;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
        KESULT 4
UPA3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation, identification and synthesis of locustamyotropin III and IV, two additional neuropeptides of Locusta migratoria: members of the locustamyotropin peptide family.", Insect Biochem. Mol. Biol. 22:447-452(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                  Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                         A novel D-1eucine-containing Conus peptide: diverse conformational dynamics in the contryphan family.";
J. Pept. Res. 54:39:39:1939;
J. SEPT. Res. 54:39:39:1939;
J. TISSUB SPECTROTION: Secreted.
J. TISSUB SPECTROTICITY: Expressed by the venom duct.
J. MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
J. SIMILARITY: Belongs to the contryphan family.
DISULPID.
2 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Locustamyotropin 3 (LOM-MT-3).
Locustamyotropin 3 (LOM-MT-3).
Locustamyotropin (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteracoidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
        Conus purpurascens (Furple cone).
Bukaryota; Metazoa; Mollusca; Gaetropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.6%; Score 18; DB 1; Length 9; llarity 75.0%; Pred. No. 1.4e+05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                          Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD RES 9 9 AMIDATION. SEQUENCE 9 AA; 1140 MW; D5AE1772C9D776C6 CRC64;
                                                                                                                                                                                                                                                                                 4 4 D-LEUCINE.
8 AA; 890 MW; 75A36767232CEB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (myotropic activity).
-!- SIMILARITY: Belongs to the pyrokinin family. PIR, A61620, A61620.
InterPro; IPRO01484; Pyrokinin.
PROSITE; PS00539; PYROKININ; 1.
Neuropeptide; Amidation; Pyrokinin.
MOD_RES.
9 9 AMIDATION.
                                                                                                                                                                                                                                                                                                                          34.6%; Score 18; DB 1; I
40.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA.
                                                                                           SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN=Clipperton Island; TISSUE=Venom;
MEDLINE=99388839; PubMed=10461743;
                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.46
2; Mismatches
                                                                                                                                                                                                                                                                                                                                        Local Similarity 40.0 les 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                 NCBI_TaxID=41690;
Leu-contryphan-P.
                                                                                                                                                                                                                                                                                                                                                                                1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                               |: :|
2 CVLLP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 PLVP 8
                                                                                                                                                  Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMT3 LOCMI
                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LMT3 LOCMI
                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
ठ
                                                                                                                                                                                                                                                                                                                                                                                                         음
```

PFVP 7

```
J. Comp. Neurol. 419:352-363(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20189894, PubMed-10723010,
Predel R., Eckert M.;
"Tagma-specific distribution of FXPRLamides in the nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                   "Plasma protein map: an update by microsequencing.";
Electrophoresis 13.707-714(1992).
-!- MISCELLANBOORS: On the 2D-gel the determined pI of this unknown protein is: 4.6, its MW is: 46 kDa.
SWISS-2DPAGE; P30089; HUMAN.
                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G., "Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach."; Peptides 18:473-478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteracidea; Dictyoptera; Blattaria; Blattoidea;
NCBI_TaxID=6978;
               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                           :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.7%; Score 17; DB 1; Length 9; 75.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
                                                                                                                                                                                                                                                             MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pa
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: Corpora cardiaca.
-!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
-!- SIMILARITY: Belongs to the pyrokinin family.
InterPro; IPR001484; Pyrokinin.
PROSITE; PS00539; PYROKININ; FALSE_NEG.
9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Corpora cardiaca;
MEDLINE=97353923; PubMed=9210163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the American cockroach.";
```

ö

o;

Gaps

.,

SEQUENCE Query Match

Best Loc Matches

à

PPK3_PERAM

RESULT 6

MOD RES

```
"Plasma protein map: an update by microsequencing.";

Electrophoresis 13:707-714(1992).

-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown

protein is: 5.05, its MW is: 37 kDa.

SWISS-2DPAGE; P30093; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Litoria rubella (Desert tree frog).

Litoria rubella (Desert tree frog).

Metazoa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae, Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus striatus (Striated cone).

Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                      MEDLINE=93092937; PubMed=1459097; Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 13; DB 1; Length 6; 66.7%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              28.8%; Score 15; DB 1; Length 9; 100.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                    5 5 9 9 9 9 9 AA; 5C14477AEB0772C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES 6 AMIDATION.
SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aust. J. Chem. 52:639-645(1999).
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                       3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arg-conopressin S.
                                                                                                                                                                                                                                                                                                                                                                         6 LVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VPL 6
      TISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EI01 LITRU
P820<u>9</u>6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONST
                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                 NON TER
UNSÜRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONO CC
P05487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
EIO1_LITRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
CONO_CONST
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OCC OCC OFF DATA
                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the American cockroach.";
J. Comp. Neurol, 419:352-363(2000).
-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Retrocerebral complex, MEDLINE=99212469; PubMed=10196736; MEDLINE=99212469; PubMed=10196736; MEDLINE=99212469; PubMed=10196736; Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.; "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach."; Insect Biochem. Mol. Biol. 29:139-144(1999).
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20189894; PubMed=10723010;
Predel R., Eckert M.;
"Tagma-specific distribution of FXPRLamides in the nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                 Periplaneta americano (Marrican Cockroach).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 20-page of plasma (Spot 18) (Fragment).
                                                                      30.8%; Score 16; DB 1; Length 8; 50.0%; Pred. No. 1.4e+05; Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%; Score 15; DB 1; Length 8; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                  8 8 AA; 884 MW; CB34176DD9D77775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA; 997 MW; 0B34177409D772C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity).
--- TISSUE SPECIFICITY: Corpora cardiaca.
--- MASS SPECTROMETRY: MW-596.5; METHOD=MALDI.
--- SIMILARITY: Belongs to the pyrokinin family.
Neuropeptide; Amidation; Pyrokinin.
MOD RES 8 AMIDATION.
--- MAIDATION.
                                                                                                                                                                                                                                                                                                                                               (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
(Pea-PK-3) (FXPRL-amide).
                                                                                                                                                                                                                                                                                          8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
Neuropeptide; Amidation; Pyrokinin
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
                                                                                          Local Similarity 50.0
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                     3 SVPLVP 8
                                                                                                                                                                                         1 SPPFAP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LVP 3
                                                                                                                                                                                                                                                                                                                                                   16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                       Pyrokinin-3
                                                                                                                                                                                                                                                                                        PPK3 PERAM P82618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UPA7 HUMAN
P30093;
```

; 0

Gaps

.,

Query Match

Matches

à

RESULT 7 UPA7_HUMAN

SEQUENCE

[2] REVIEW.

```
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(11997).
-! SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Allergen Pus s 13596* (Fragment).
Fusarium solani (subsp. pisi) (Nectria haematococca).
Fukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
                                                                                        Cydia pomonella (Codling moth).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Bodopterrygota, Lepidoptera, Glossata, Ditrysia,
Tortricoidea, Tortricidae, Olethreutinae, Cydia.

NCBI_TaxID=82600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.1%; Score 12; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          23.1%; Score 12; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=IARI 3596; TISSUB=Mycelium;
Verma J., Gangal S.V.;
Submitted (JUL-1997) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                         8 8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 8 8A; 898 MW; C372C441F5B69041 CRC64;
ALL6_CYDPO STANDARD; PRT; 8 AA. P82157; 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                  TISSUE=Larva;
MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60...
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LPL 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
FUSS FUSSO
ID FUSS FUSSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UPA1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE.
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P300E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
UPA1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (contraction)
                                   Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D., Gray W.R., Olivera B.M.;
Threertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms.";
J. Biol. Chem. 262:15821-15824(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
Catch-relaxing peptide (CARP).
Mytilus edulis (Bunssel).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloidea; Mytilidae; Mytiluse, Mytiluse).
                                                                                                                                                                           Gray W.R., Olivera B.M., Cruz L.J.;

Gray W.R., Olivera B.M., Cruz L.J.;

L. Annu. Rev. Biochem. 57:665-700(1988).

-! FUNCTION: Targets Sorgessin-oxytocin related receptors.

-! FUNCTION: Targets Species of the venom duct.

-! SINLIARITY: Expressed by the venom duct.

-! SINLIARITY: Eslongs to the vasopressin/oxytocin family.

R PIR; B26495; B28495.

InterPro; IPR000981; Neurhyp_horm.

R Pfam; PF00220; hormone4; 1.

R PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

R HORMONE; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88052022; PubMed=3676797;
MEDLINE=88052022; PubMed=3676797;
Minacka T., Kubota I., Takabatake I., Kawahara A., Shimamoto N., Muncoka Y.;
"Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
Brain Res. 422:374-376(1987).
-!- FUNCTION: This peptide exhibits both potentiating (contract and inhibitory (relaxation) effects on the anterior byssus retractor muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 12; DB 1; Length 7; Pred. No. 1.4e+05; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 13; DB 1; Length 9; illarity 100.0%; Pred. No. 1.40+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              9 9 AMIDATION.
9 AA; 1031 MW; 17EB176EB4540050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION
                       MEDLINE=88058932; PubMed=3680228;
                                                                                                                                                              MEDLINE=89024586; PubMed=3052286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Conservative
                                                                                                                                                                                                                                                                                                                                                                                               90
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
2; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 1; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMPML 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SVPLV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CI 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ı
U
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
```

RESULT 10

ઠે 셤 ; 0

Gaps

.; 0

0; Indels

ö

Gaps

;

0; Indels

RESULT 11

g

```
3 SVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 secs
                                                                                                                 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SEQUENCE
                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search comp
Job time :
            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P8330;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FMRPamide-like neuropeptide FLP5 (SMPSIRIRF-amide).
FMRPamide-like neuropeptide FLP5 (SMPSIRIRF-amide).
Eukaryota, Metazoa, Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Bucarida; Decapoda; Dendrobranchiata; Penaeoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                      TIŜSUE-Plasma;
MEDLINE-93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                       23.1%; Score 12; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12; DB 1; Length 9;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0007218; P:neuropeptide signaling pathway; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION.
B60B07340735A766 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    8 AA; 944 MW; C01772C455BB06DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 66.7%;
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 9
9 AA; 1106 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penaeidae; Penaeus.
NCBI_TaxID=6687;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Eyestalk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :||
5 NVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FARS PENMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            family
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٣
                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                          NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
FARS PENNO
AC PRARS PI
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DT 28-FEB-
DC BUMBlack
OC BU
                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

9 A.A.

PRT;

STANDARD;

RESULT 15 FLA2_TREHY ID FLA2_TREHY

m

```
o;
                                                                                                                                                                                                                                                                                                                                                                                                          MEDITIRE 93139764; PubMed=1487733;

Koopman M.B.H. Baats B., van Vorstenbosch C.J.A.H.V.,

Koopman M.B.H. Baats B., van Vorstenbosch C.J.A.H.V.,

Van der Zeijst B.A.M., Kusters J.G.;

"The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are composed of two sheath proteins and three core proteins.";

J. Gen. Microbiol. 1381:2697-2706(1992).

-!- FUNCTION: Component of the outer layer of the flagella.

-!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE THAT CONTAINS THREE PROTEINS FLABI (37 kDa), FLABS (34 kDa) AND FLAB3 (32 kDa).
                                                                                                                                                                           Treponema hyodysenteriae (Serpulina hyodysenteriae).
Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
NCBI_TaxID=159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 1; Length 9;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA; 1129 MW; 855A19C68B4772D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Periplasmic flagellum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: September 5, 2004, 11:04:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Flagellum; Periplasmic.
```

This Page Blank (uspto)

```
Q9p8e5 kluyveromyc Q42564 fugu rubrip Q56140 streptococc Q8ay15 carassius a Q8aum7 carassius a Q7x6a3 zea mays su P9333 lycopersico 002831 oryctolagus Q9try3 sus sp. ins Q16220 homo sapien Q9umf3 homo sapien Q9umf3 homo sapien Q9umf3 curs sapien Q9umf3 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      September 5, 2004, 10:59:47; Search time 31.667 Seconds (without alignments) 89.674 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                       840
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                          1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9PRES
042564
056140
Q8AYLS
Q8AUM7
Q7X6A3
P92233
O02831
Q9TRY3
Q9UMF3
Q9UMF3
Q07V624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          078225
0988J8
035953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sparchea:*
sparchea:*
spbacteria:*
spbunci:*
spinwan:*
spinvertebrate:*
spondanelle:*
spondanelle:*
spprodent:*
sp
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                   US-09-761-636A-14
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL 25:*
                                                                                                                                                                                                                                                          1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11199
11199
11199
11199
11199
11199
11199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
```

09s8j8 oryza sativ 035953 mus musculu

007354 synechococc Q9x3k1 prochlorococ P8352 lactobacill Q9trx8 bos anivas P8356 sepia offic Q67113 influenzavi Q49534 mycoplasma O3256 escheriola Q8wfr5 diadema pau Q8kfr5 diadema pau Q8kfr5 mus musculu Q9p40 mus musculu Q9p40 mus musculu Q9p40 mus musculu Q9p40 mus musculu Q9e8g5 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b Q9e8g1 beet soil-b	09e8q0 09e8q7 09dsn6 09e8q6	9 AA. ce update) cion update) cotina; Saccharomycetes;	Freire-Picos M.A.; Conal regulation: similarities Siae HIS4 gene."; CD767 CRC64; DB 3; Length 9; 16+06; 0; Indels 0; Gans 0;	
7 2 007354 8 2 09X351 8 2 09X351 8 6 09TRX8 8 6 09TRX8 7 12 067113 8 2 04534 9 12 09584 8 11 099P4 8 12 09E802 8 12 09E802 8 12 09E802 8 12 09E802 8 12 09E802 8 12 09E803 8 12 09E803	112 Q9E8Q0 112 Q9E8Q7 112 Q9E8Q7 112 Q9ESQ6 112 Q9E8Q6 112 Q9E8Q6	ARY; PRT; 9 AA. el. 15, Created) el. 15, Last sequence update) el. 16, Last annotation update) nt). (Yeast). (Yeast). comycota; Saccharomycotina; Sacciaccharomycetaceae; Kluyveromyces	RN 11) RN 11 RN 11 RN 121 RC STRAIN=NRRL-Y1140; RX MEDLINE=99448382; PubMed=10518937; RA Lamas-Maceiras M., Esperanza Cerdan E., Frei RT "Kluyveromyces lacxtis H184 transcriptional RT and differences to Saccharcomyces cerevisiae RL FEBS Lett. 458:72-76(1999). DR EMBL, AJ23494; CAB87125.1; - FT NON TER 9 SQ SEQÜENCE 9 AA; 1015 NW; 5770D2D772D2D767 Query Match Best Local Similarity 60.0%; Pred No. 18-06 Macches 3; Conservative 2; Mismatches	; PRT; 7 05, Created)
4444 111111111111111111111111111111111	13 25.0 8 13 25.0 8 13 25.0 8 13 25.0 8 13 25.0 8 13 25.0	PRELIMINARY  -2000 (TrEMBLrel2001 (TrEMBLrel. rotein (Fragment) romyces lactis (Y comyces lactis (X ota; Fundi; Ascom och; Fundi; Ascom axID=28985;	CE FROM N.A.  =NRAL-Y1140;  E=99448382; PubMe Maceiras M., Espe eromyces lacxtis fferences to Sacc fferences to Sacc ett. 458:72-76(19 AJZ38494; CAB8712 R AJZ38494; CAB8712 CE 9 AA; 1015 ch CS 9 AA; 1015 CS 9 AA; 1015 CS 3, Conservativ 60 3; Conservativ 60 3; Conservativ 60	4 VPLVP 8 2 LPVVP 6 PRELIMINARY 1998 (Trembleel.
1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	ብ ብ ብ ብ ብ በ ር ራ ቁ ብ	RESULT 1 09P8E5 1D 09P8E5 AC 09P8E5 DT 01-0CT DT 01-MAR DE HIS4 PI GN HIS4 PI GN Kluyve: OC ENKARY OC ENKARY OC SACCHAIN	RN 11 RP SEQUEN RC STRAIN, RA MEDLINI RA LEMBALINI RT "KLUYYY RT and dil RL EMBL, I PR EMBL, I FT NON TEE SQ SEQÜENI QUETY MATC BEST LOCAL	Oy 4 VDL

.. 0

Gaps

```
Trinudakova A.V., Kishida M., Wood E., Callard G.V.;
Trinudakova A.V., Kishida M., Wood E., Callard G.V.;
"Promoter characteristics of two CYP19 genes differentially expressed in the brain and ovary of teleost fish.",
J. Steroid Biochem. Mol. Biol. 0:0-0(2001).

BMBL; AF324895; AAN32616.1; -.

EMBL; AF324896; AAN32617.1; -.

NOW TER 9 9 9

SEQÜENCE 9 AA; 961 MW; C49E76D7272B187D CRC64;
                                                                                                                                      SEQUENCE FROM N.A. Tribulda M., Wood E., Callard G.V.; Trohoudakova A.V., Kishida M., Wood E., Callard G.V.; Trohoudakova A.V., Kishida M., Wood E., Callard G.V.; Promoter characteristics of two CYP19 genes differentially expressed in the brain and ovary of teleost fish."; J. Steroid Biochem. Mol. Biol. 0:0-0(2001).

EMBL, #87324897; ANN32618.1; -.

NON_TER. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
                       Actinopterygii, Meopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.
NSBL TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays subsp. mays (maize).
Sukaryota, Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.6%; Score 18; DB 13; Length 9; 75.0%; Pred. No. 1e+06; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                            Score 18; DB 13; Length 9; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                           9 AA; 1060 MW; C49E76D7272B040D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                0; Mismatches
   Cytochrome P450 aromatase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome P450 aromatase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                          34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Goldfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Fragment)
                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carassius auratus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOPC 9
                                                                                                                                                                                                                                                                                                                                                                  LVPC
                                                                                                                                                                                                                                                                                                                                                                                                  LOPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoamylase
                                                                                                                                                                                                                                             NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  ي
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7X6A3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8AUM7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYP19A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7X6A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBAUM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8AUM7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7X6A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò,
                                                                                                                                                                                                                         Plummer N.W., McBurney M.W., Meigler M.H.,
"Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.";
Elol. Chem. 272:24008-24015(1997).
EMBL, U97673; AAR80916.1, ---
GO, GO:0005216; F:ion channel activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Constable A., Mollet B.;
"Isolation and characterisation of promoter regions from Streptococcus thermobilus.";
FEMS Microbiol. Lett. 122:85-90(1994).
EMBL: X78210; CAA55045.1; -
NON TER 8 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae, Takifugu.
 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                  36.5%; Score 19; DB 13; Length 7; 100.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.5%; Score 19; DB 2; Length 8; 100.0%; Pred. No. 1e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA; 846 MW; ED086772D5B045B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=97442476; PubMed=9295353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95047254; PubMed=7958782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q56140;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STP6 protein (Fragment).
01-JAN-1998 (TrEMBLrel. 01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VPLV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VPLV 4
                                                                                                                                                                                                                                                                                                                                   Conic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8AYL5;
01-MAR-2003
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                  SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                TER
```

056140

RESULT 3 056140

Matches

ð

g

ö

Gaps

Q8AYL5

검검검당

RESULT 4 QBAYLS

Matches

ò

· 0

. 0

```
Shimasaki S., Gao L., Shimonaka M., Ling N., "Isolation and molecular cloning of insulin-like growth factor-binding
                                                                                                                                                                  "Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";
Matrix Biol. 15:39-47(1996).
EMBL; S83371; AAD14433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94320083; PubMed=8044796;
Nagalla S.R., Spindel E.R.;
"Functional analysis of the 5'-flanking region of the human gastrin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI TaxID=9826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukanyota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                  Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 8; 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%; Score 16; DB 6; Length 8; 100.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                     NON TER 1 1 SQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      850 MW; 9FB2CEA37EA7687D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                 30.8%; Score 16; DB
100.0%; Pred. No. 1e+
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                      MEDLINE=96377339; PubMed=8783186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92049376; PubMed=1719383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Endocrinol. 5:938-948(1991).

NON TER 1 1

NON TER 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA;
           NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 PC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
PC
                                                                                                                                                                                                                                                                                  Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-6
                                                                                                                                              Vuorio E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  016220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9TRY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q16220
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               016220
           SO RETARAN SERVICE SO SERVICE SO SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . . ., IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (Tomato).
Bukaryota; Viridijalnate; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                        STRAIN=cv. 38-11, and cv. A632;
Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
Buckler E.S. IV.;
"Dissection of maize starch production by candidate gene
association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-97351561; PubMed-9207643;
Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
"Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pro alpha I type III collagen protein (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U75692; AA49682.1; -...GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase GO; GO:0016829; F:1yase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                        32.7%; Score 17; DB 10; Length 9; 66.7%; Pred. No. 1e+06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%; Score 16; DB 10; Length 7; 80.0%; Pred. No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last amnotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                                                                                                            Submitted (MAY-2003) to the EMBL/GenBank/DDBU databases. EMBL, AY290305; AAP45331.1; -. EMBL; AY290311; AAP45337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                         9 AA; 976 MW; DF9BCEA76736C6DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 828 MW; 71B412C7377415D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Lycopersicon esculentum).";
Plant Mol. Biol. 34:275-286(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel. 03, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               002831;
01-JUL-1997 (TrEMBLrel. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 2; Conserv
                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SVPLV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4081;
NCBI_TaxID=4578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 VPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jo,
Lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                   NON TER
```

P93233

RESULT 7 P93233

Best Loc Matches

à

0

Gaps

.;

002831

002831 1D 002831 1D 000 000 000 000 000 000 000

RESULT 8

Matches

à g ÷.

Gaps

;

```
/ Match 30.8%; Score 16; DB 12; Length 9; Local Similarity 100.0%; Pred. No. 1e+06; les 2; Conservative 0; Mismatches 0; Indels
    9 9 9 9 9 9 9 AA; 1154 MW; 8B6A3EA764541415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lymphocyte antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosomes.";
Genet. Res. 50:137.146(1987).
EMBL; L38589; AAA5723.1; -.
                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100.v
Thes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.v.
Loc 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 PSIP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LVP 8
                                                                                                                                             8 PC 9
                                                                                                                                                                                     ,
                                                                                                                                                                                     Z-
    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              078225
                                                                                                                                                                                                                                                                                          Q07624
Q07624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
078225
                                                                                                        Matches
                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
    FT
                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
MEDLINE=97473511; PubMed=9332365;
Finger L.R., Pu U., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
Finger L.B., Pu U., Wasserman R., Vibhakar R., Louie E., Hardy R.R.,
Burrows P.D., Billips L.G.;
"The human PD-1 gene: complete cDNA, genomic organization, and
developmentally regulated expression in B cell progenitors.";
Gene 197:177-187(1997).
BMBL; U64864; AAC51774.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                               Gaps
releasing peptide gene in small cell lung carcinoma cell lines."; Cancer Res. 54:4461-4467(1994).
EMBL; S73265; AAD14116.1; -.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
NON TER 9 9 SEQÜENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLIRE=21580659; PubMed=11724134;
Bleraky N.Z., Kania S.A., Potgieter L.N.;
"The ovine respiratory syncytial virus F gene sequence and its diagnostic application.";
J. Vet. Diagn. Invest. 13:455-461(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses, šsRNA nėgativė-strand viruses, Mononegavirales,
Paramyxoviridae, Pneumovirinae, Pneumovirus.
NCBI_TaxID=28869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA; 1067 MW; DD4A676DC6C76046 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Matrix protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
PD-1 protein (Fragment).
                                                                                                                                                                  Query Match 30.8%; Score 16; DB 4; Best Local Similarity 75.0%; Pred. No. 1e+06; Matches 3; Conservative 1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 4;
Pred. No. 1e+06;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ovine respiratory syncytial virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ISVPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MQIPQAP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=9606;
                                                                                                                                                                                                                                                     4 VPLV 7
                                                                                                                                                                                                                                                                                            6 LPĽV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8QVD3
Q8QVD3;
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9UMF3;
                                                                                                                                                                                                                                                                                                                                                                                                Q9UMF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
Q8QVD3
                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                             Q9UMF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT TO DT 
                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
        RT DR DR DR DR DR DR DR SO
                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                              g
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         MEDLINE=93010967; PubMed=1327749;
MEDLINE=93010967; PubMed=1327749;
Donze O., Spahr P.F.;
"Rolle of the open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBO J. 11:3747-3757(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mūs musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIM=CROM435; TISSUD=Kidney;
MEDLINE=80084418; PubMed=3692165;
Golubic M., Budimir O., Schoepfer R., Kasahara M., Mayer W.E.,
Figueroa F., Klein J.;
"Nucleotide sequence analysis of class II genes borne by mouse t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.8%; Score 15; DB 15; Length 7; 50.0%; Pred No. 1e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.8%; Score 15; DB 7; Length 9; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                          Rous sarcoma virus (strain Prague C).
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA; 1143 MW; 9E681772C729C33A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X67587; CAA47862.1; -. SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;
7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
```

|||| | LVP 7

q

```
[1] —

SEQUENCE.

MEDLINE=95102521; PubMed=7804141;

Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;

Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;

"Isolation and characterization of oryzatensin: a novel bioactive peptide with ileum-contracting and immunomodulating activities derived from tea albumin.";

Biochem. Mol. Biol. Int. 33:1151-1158(1994).

Gramene; Q9S8J8; ---

SEQUENCE 9 AA; 1093 MW; OEBC67377B56877B CRC64;
                                                                                                                9988J8 PRELIMINARY; PRT; 9 AA.
998BJ8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
07XZATENSINA-BIOACTIVE peptide.
07XZA BALIVA (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
NTBLTAXID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.8%; Score 15; DB 10; Length 9; Best Local Similarity 50.0%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 1; Indels
RESULT 15
1095878
10 095874
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10 01-00
10
```

Search completed: September 5, 2004, 11:05:43 Job time : 32.6667 secs

|: | 3 PMYP 6 5 PLVP 8

δ a

ò

0; Gaps

This Page Blank (uspto)

```
7; Search time 37.3333 Seconds (without alignments) 68.114 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                           231240
 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                        1586107 seqs, 282547505 residues
GenCore version
Copyright (c) 1993 - 2004
                                                                                                5, 2004, 10:56:37
                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                US-09-761-636A-14
52
                                                                                                                                                                                                     1 CISVPLVPC 9
                                                                                                    September
                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                        Searched:
                                                                                                Run on:
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* 1: genesecm10802 geneseqp2004s:* E 4 5 6 7 8 Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	DB ID Description	4 AAU04533 VEGF base	ABG35134 Abg35134	ABB46931 Abb46931	2 Abq60522	ABR56920 Abr56920	AAY84998 Aay84998	ADC44293	3 AAY63242 Protocadh	AAE07204 Aae07204	AAM24655	ABG35050	AAR95843 Aar95843	AAY84999 Aay84999	ADC44308	AAY03909		ABP21743 Abp21743	AAU94456	AAU94653 Aau94653	ADC44488 Adc44488	ADC59359 Adc59359	2 AAW85926 Rodent IL	ABP99702 Human s		
	Query Match Length	6	σ	σ	6	თ	7	7	σ	Q	σ	6	5	S	S	9	6	σ	σ	o,	6	6	9	9	7	
dю	Query Match	100.0	51.9	51.9	Ξ.	51.9	50.0	50.0	50.0	50.0	20.0	50.0	48.1	48.1	48.1	46.2	46.2	46.2	46.2	46.2	46.2	46.2	44.2	44.2	44.2	
	Score	52	27	27	27	27	26	26	26	26	56	26	25	25	25	24	24	24	24	24	24			23	23	
	Result No.	1	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Aar58417 Partial p		Aar58418 Partial p	Aaw99327 Human IgG	Aay10322 T cell ep	Aaw99853 HIV-1 gpl	Aay47758 Immunogen	Aay45765 Immunogen	Aay45766 Immunogen	Aay48998 Membrane	Aay51358 MHC type	Aab36017 Human bet	Aab27093 Plasmodiu	Aab61826 Human Ig	Aae26894 Linker pe	Abg35060 Angiostat		Abq60516 Selective	Abg80004 MHC class
2 AAR58417	2 AAR58415	2 AAR58418	2 AAW99327	2 AAY10322	2 AAW99853	2 AAY47758	2 AAY45765	2 AAY45766	2 AAY48998	3 AAY51358	3 AAB36017	3 AAB27093	4 AAB61826	5 AAE26894	5 ABG35060	5 ABG35128	5 ABG60516	5 ABG80004
23 44.2 8		23 44.2 8				23 44.2 9		23 44.2 9	23 44.2 9	44	23 44.2 9	23 44.2 9	3 44.2	44	44.2	44.2	.2	23 44.2 9
26	- 80	29 2	30	31 2	32	33	34	35 2	36 ,					41 2	7	43 2	44 2	45

## ALIGNMENTS

VEGF based monocyclic peptide 11. AAU04533 standard; peptide; 9 AA. (first entry) 26-SEP-2001 AAU04533; RESULT 1 AAU04533 ID AAU0 

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic

1. 9 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond WO200152875-A1. 26-JUL-2001.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533.

Cendron A; ŝ Stacker Hughes RA, WPI; 2001-442248/47. Achen MG,

(LUDW-) LUDWIG INST CANCER RES

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

peptide loop fragment from an exposed loop of a growth factor protein and cyclising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, covariant and the condition of the cyclisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cirauma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascular sequelae, hypertension induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VGGF, VGGF, cor -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy 

Sequence 9 AA;

100.0%; Score 52; DB 4; Length 9; 100.0%; Pred. No. 1.40+06; cive 0; Mismatches 0; Indels Conservative 1 CISVPLVPC 9 CISVPLVPC 9 Query Match Best Local Similarity 9 Matches a ઠ

ö

Gaps

;

ABG35134 standard; peptide; 9 AA. RESULT 2 ABG35134

Pancreatic islet targeting peptide #10. 15-JUL-2002 (first entry) ABG35134; 

Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiatherosclerosclero; antidiabetic; antibacterial; diabetes mellitus; inflammatory disease; arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection

Unidentified.

WO200220722-A2.

14-MAR-2002.

07-SEP-2001; 2001WO-US027702

08-SEP-2000; 2000US-0231266P.

(TEXA ) UNIV TEXAS SYSTEM.

Pasqualini R; Arap W,

WPI; 2002-383050/41.

Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.

Claim 56; Page 288; 298pp; English.

```
.
0
                              targeting peptides. The method comprises exposing a sample from an organ, tissue or cell type of interest, to a phage display library and recovering phage bound to the sample (the phage expresses targeting peptides). The peptides identified by the method of the invention may have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic, antiatheresclerotic, antidabetic, antibacterial and antiviral activities. The methods and composition are useful for identifying targeting peptides and one or more receptors for a targeting peptides. The targeting peptides are used for selective delivery of therapeutic agents, including gene therapy vectors and fusion proteins, to specific organs, trissues, or cell types in subject. The targeting peptide may also be used for treating diseases such as diabetes mellitus, inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodyin's diseases. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, comprising a modulating agent comprising a desmosomal cadherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cadherin CAR sequence and/or a polynucleotide encoding a polypeptide that comprises a desmosomal cadherin CAR sequence can analogue. The modulating agents have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
                 invention relates to a novel method for identifying disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 27; DB 5; 1
Pred. No. 1.4e+06;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desmocollin-2 CAR cyclic peptide 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gour BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 23; Page 111; 127pp; English.
                                                                                                                                                                                                                                                                                                                                targeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB46931 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-2000; 2000US-00535852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2001; 2001WO-1B001400.
                                                                                                                                                                                                                                                                                                                                                                                                             51.9%;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.00,
Best Accaservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaschuk OW, Symonds JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-025778/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CMSSPGVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CISVPLVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200172956-A2.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB46931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB4693
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

.. 0

Gaps

·.

3; Indels Length 9;

Score 27; DB 5; 1 Pred. No. 1.4e+06;

51.9%;

1; Mismatches

5; Conservative

Query Match Best Local Similarity Matches 5; Conserv

σ

1 CMSSPGVAC

셤

ò

1 CISVPLVPC

```
Targeting peptide; cancer; arthritis; diabetes; inflammatory disease; atherosclerosis; autoimmune disease; bacterial infection; apoptosis; viral infection; cardiovascular disease; degenerative disease; ischaemia; inflammaton; macular degeneration; antiinflammatory; antiidiabetic; cardiovascular; immunomodulator; antibacterial; antiviral; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       delivery to an organ or tissue, particularly for treating a disease, e.g. cancer, inflammatory or autoimmune diseases, infections or cardiovascular
  are used to
immunosuppressive, cytostatic and antiapoptotic activity and are used to facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Targeting peptides identified by phage display, useful for targeting
                                                                                                                              ·.
                                                                                                                             4; Indels
                                                                                                  Score 27; DB 5; Length 9;
Pred. No. 1.4e+06;
                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 121; 317pp; English.
                                                                                                                                                                                                                                                                                                                      Selective targeting peptide #197.
                                                                                                                                                                                                                                             ABG60522 standard; peptide; 9 AA.
                                                                                                 51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2001; 2001WO-US027692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasqualini R;
                                                                                                                                                     6
                                                                                                                                                                     ||:
CIAFATTPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-415731/44.
                                                                                                                                                     1 CISVPLVPC
                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200220769-A1
                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy
                                                                                                                                                                                                                                                                                            30-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                    ABG60522;
                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arap W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease.
                                                                                                                             Matches
                                                                                                                                                                                                                  8X333333
                                                                                                                                                     ð
                                                                                                                                                                           입
```

Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental delivery; terapy all pacenta; adipose; pancreatic; beta-1 integrin; beta-5 integrin; spleen; aminopeptidase A.

Arap W, Kolonin MG;

Pasqualini R,

(TEXA ) UNIV TEXAS SYSTEM.

30-AUG-2002; 2002WO-US027836. 07-SEP-2001; 2001WO-US027692.

WO2003022991-A2

20-MAR-2003

musculus

Mus

Synthetic

Pancreatic targeting peptide SEQ ID NO:137.

(first entry)

30-JUL-2003

ABR56920;

ABR56920 standard; peptide; 9 AA

ABRS6920

. 0

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipaemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teartogenic activity. ABR56806 to ABR56227 and ACC79106 to ACC79111 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.9%; Score 27; DB 6; Length 9; 55.6%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 9; Page 114; 247pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-371749/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 5, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPLVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CMSSPGVAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subject
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
```

in size useful for targeting delivery to an organ or tissue, particularly disease, adisease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with inflammation or macular degeneration. Furthermore, the peptide is useful for diagnosing the diseases cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60326-ABG60574 represent selective targeting

peptides of the invention

Sequence 9 AA

The invention relates to an isolated peptide of 100 amino acids or less

endothelial cell binding protein; ECBP; anti-tumour; cytostatic; vasotropic; antipsoriatic; dernatological; ophthalmological; antidiabetic; antiathritic; vulnerary; antiulcer; antinflammatory; antibacterial; gynaecological; angiogenesis.

cell binding peptide SEQ ID NO:21.

Endothelial

(first entry)

18-DEC-2003

ADC44293;

```
The present sequence represents an endothelial cell-binding peptide motif. The peptide may be identified using the method of the invention. The specification describes a method for generating a peptide having a selected biological activity. The method comprises displaying the selected biological activity. The method comprises displaying the peptide display library, and using affinity selection to enrich the copulation display packages for those containing peptides which have copulation of specificity to the target cell. The method may be used in the selection of peptides having effects on cell proliferation, described shich have anti-proliferative activity with respect to one or more types of cells, peptides with (anti-) angiogenic activity, anti-cincetive peptides (e.g. which are active as anti-fungal or anti-cincetial), receptor protein effectors, and ligands for orphan receptors for which no ligand-receptor and channel interactions for cell surface-localized receptors and channels
                                                                                                                                                                Endothelial cell-binding peptide, Genetic display package, peptide display library, affinity selection, population display package, cell proliferation, cell differentiation, cell death, cell migration, anglogenic activity, infective peptide, anti-fungal; anti-bacterial; receptor protein effector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generating a peptide with a selected biological activity useful for identifying endothelial inhibitors and peptides with anti-angiogenic activity by combining peptide display libraries in a display and a
                                                                                                                                Amino acid sequence of an endothelial cell-binding peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 3; Length 7;
Pred. No. 1.4e+06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 42; 86pp; English.
                 AAY84998 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US024276
                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00174943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                             21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Syuris J, Morris AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-339649/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                         WO200023465-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretion mode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        19-0CT-1998;
                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                              27-APR-2000
                                                       AAY84998;
AAY84998
```

Novel synthetic or recombinant polypeptide useful for promoting, reducing proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.

Claim 3; SEQ ID NO 21; 126pp; English

Tsaioun K;

Morris AJ,

Lamphere L,

Gyuris J,

WPI; 2003-482072/45.

(GPCB-) GPC BIOTECH INC.

01-NOV-2002; 2002WO-US035258. 01-NOV-2001; 2001US-0334822P.

WO2003037172-A2

Synthetic

08-MAY-2003.

```
The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell peptide of the invention has anticumnary, cytostatic, vasotropic, antipsoriatic, dermatological, cumour, cytostatic, vasotropic, antipsoriatic, dermatological, antiulcer, autinflammatory, antidabetic, antiarthritic, vulnerary, antiulcer, cophthalmological, antidatestial, and gynaecological activity. The peptide is useful for promoting, reducing the proliferation and/or migration of the preferably the peptide, to promote proliferation and/or migration of the treated cells, and for reducing or promoting angiogenesis, by treating the cells with an BCBP antagonist, which is preferably the peptide of the invention is also useful for manufacturing a medicament for promoting angiogenesis, by admixing an ECBP agonist or ECBP antagonist to promote or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis. ECBP sequences are useful for promoting or angiogenesis. ECBP sequences are useful to alter the infectivity spectrum of a vizal particle. The present sequence represents an ECBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 7; 1
Pred. No. 1.4e+06;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY63242 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIPLVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY63242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY63242
EXAXAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   음
```

ö

Gaps

.. 0

5,

4; Conservative

œ SVPLVP

m

6 g ADC44293 standard; peptide; 7 AA.

RESULT 7 ADC44293

```
WPI; 2000-038791/03.
                                Disulfide-bond
                                                                                                                                                 Sequence 9 AA;
                                                                  Blaschuk OW,
                         Homo sapiens.
                                    WO9957149-A2
                                              05-MAY-1999;
                                                  05-MAY-1998;
                                                    06-NOV-1998;
20-JAN-1999;
                                                         08-MAR-1999;
                                         11-NOV-11999,
                       Synthetic
```

```
The invention relates to colostrinin peptide fragments which are useful, inter alia, in the treatment of chronic disorders of the immune system and the central nervous system colostrinin peptides are used as a medicament in the treatment of neurological disorders e.g., dementia, neurodegenerative disorders e.g., Altheimer's disease, motor neuron disease e.g., Parkinson's disease, mental disorders e.g. psychosis and neurosis, in acquired immunlogical deficiencies, chronic bacterial and viral infections and diseases characterised by the presence of beta-dults and senile persons, who have been subjected to chemotherapy or have suffered from cachexia or weight loss due to the chronic disease.

Colostrinin peptides are also used as food additives and as an auxillary withdrawal treatment for drug additicts, after a period of detoxification and in persons dependent on stimulants. Colostrinin peptides are used to
                                                                                                                                                                                                                                                                                                      Colostrinin, nootropic, neuroprotective, immunomodulatory, antibacterial, Parkinson's disease, Alzheimer's disease, mental disorder, food additive, central nervous system disorder, weight loss; beta-amyloid plaque, psychosis; neurosis; cachexia; motor neuron disease; acquired immunological deficiency; neurological disorder; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide useful as an interalia in the treatment of e.g. disorders of the immune system and the central nervous system comprises ten amino-terminal amino acid sequence derived from peptides present in colostrinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare antibodies and to treat emotional disturbances, e.g. emotional disturbances of psychiatric patients in a state of depression. These colostrinin peptides improves the development of immune system in a new born child and to correct the immunological deficiencies in a child. The present sequence is modified colostrinin cyclic peptide #10 related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "N-terminal acetyl; this residue forms a cyclic
linkage with Ser found at the C-terminal end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 4; Length 9;
Pred. No. 1.48+06;
1; Indels
                                                                                                                                                                                                                                                  Modified colostrinin cyclic peptide #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                       AAE07204 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 9; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGE-) REGEN THERAPEUTICS PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JAN-2000; 2000GB-00001825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JAN-2001; 2001WO-GB000329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.1%;
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488775/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiviral; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155199-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georgiades JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic,
                                                                                                                               AAE07204;
            RESULT 9
                                           AAE07204
                                                                                                                               The present invention describes cadherin modulating agents (MA)

Comprising peptides which comprise a nonclassical cadherin cell adhesion

Comprising peptides which comprise a nonclassical cadherin cell adhesion

Comprising peptides which comprise a nonclassical cadhering

Comprising delivery of a drug to a tumour in a mammal, treating cancer in

commal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in

commal, inhibiting metastasis of a cancer in a mammal, inhibiting

compressing cell, preventing or treating obesity in a mammal, simulating

compressing cell, preventing or treating obesity in a mammal, simulating

compressing cell, preventing or treating a demyelinating neutrological disease,

contral nervous system, treating a demyelinating synaptic stability in

conclassical cadherin-expressing cells, inhibiting synaptic stability in

conclassical adhering pregnancy in a mammal, required for can also be used for treating e.g. psoriasis, arthritis, age

conclassical adherin and pazzillal to AAV64572 represent specifically claimed peptides, and

AAV60592 to AAV64572 represent specifically claimed peptides, and

conclassical cadherin or prevention and diagnosis and in bioreactors

AAV60592 to AAV64572 represent specifically claimed peptides, and

conclassical cadhering the conclassical cadhering e.g. psoriasis, and pazzillal the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the concerns of the conc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
Modulation; nonclassical cadherin mediated cell adhesion, CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin, cadherin-5; cadherin-6; cadherin-7; cadherin-12; cadherin-15; T-cadherin; PB-cadherin; cadherin-12; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglain; desmocollin; alcium binding; cancer; tumour; obesity; rhemmatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 26; DB 3; 1 44.4%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 84; Page 201; 252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00187859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-CA000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00073040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00264516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :: || |
CFALDLVTC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
```

.; 0

Gaps

.;

1 CISVPLV 7

à

Query Match

Matches

à g Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus; inflammatory disease; arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.

Endostatin targeting peptide #49.

(first entry)

15-JUL-2002

ABG35050;

```
The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific peptide fragments of the protein. 83P5G4 exhibits prostate specific cypression in normal adult tissue, but it is also abservantly expressed in many cancers including tumours of the prostate, testis, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, colon and lung The 83P5G4 polymucleotide, its related protein and peptide fragments and specific PCR primers are therefore useful for diagnosing and treating cancer. A vector comprising a polymucleotide channespecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polymucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that expresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and continue and to thereby detect the presence of cancerous cells
                                                                                                                                                                                                                                                                           83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; panorceas; colon; lung; serum; cytostatic; gene therapy, antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; utine; uterus; rectum; scomach; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated 83P5G4-related protein useful as a diagnostic and/or therapeutic agent in multiple cancers such as prostate, bladder and bone
                                                                                                                                                                                                                                      Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 26; DB 4; Length 9; 50.0%; Pred. No. 1.48+06; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Challita-Eid PM, Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 15; Page 77; 112pp; English.
                                                                                                                     AAM24655 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-2001; 2001WO-US004426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-2000; 2000US-0181261P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jakobovits A;
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UROG-) UROGENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Afar DEH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514669/56.
|::|||
1 CLPLPLV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200159115-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitchell SC,
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                 04-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RS,
                                                                                                                                                            AAM24655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hubert
                                                                                                  AAM24655
                                                                                                                                                          g
```

Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101. 07-SEP-2001; 2001WO-US027702

WO200220722-A2 Unidentified

14-MAR-2002

(TEXA ) UNIV TEXAS SYSTEM.

Arap W, Pasqualini R; WPI; 2002-383050/41

```
This invention relates to a novel method for identifying disease

targeting peptides. The method comprises exposing a sample from an organ,

tissue or cell type of interest, to a phage display library and

recovering phage bound to the sample (the phage expresses targeting

beptides). The peptides identified by the method of the invention may

be to recovering phage bound to the sample (the phage expresses targeting

controlled to immunosuppressive, anti-inflammatory, antiarthritic,

antiatherosolerotic, antidiabetic, antibacterial and antiviral

activities. The methods and composition are useful for identifying

cartivities. The methods and composition are useful for identifying

cartivities are used for selective delivery of therapetuic agents,

including gene therapy vectors and fusion proteins, to specific organs,

tissues, or cell types in subject. The targeting peptide may also be used

for treating diseases such as diabetes mellitus, inflammatory diseases,

cartivities, atherosolerosis, cancer, autoimmune diseases, bacterial and

cartivities in control and Hodgkin's disease. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26, DB 5, Length 9, Pred. No. 1.4e+06; 1, Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 56; Page 252; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          targeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR95843 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPLVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |:| |
CRSLPPVRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR95843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
AAR95843
ID AAR95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

ö

Gaps .. 0

ABG35050 standard; peptide; 9 AA.

RESULT 11 ABG35050

2 ISVPLVPC 9

ð

: :|| || 2 LPLPLRPC

```
growth factor-1 (169-1) mutens of the invention. This sequence represents the N-terminal residues 63-67 of the IGF-1 mutein C67. The wild type IGF-1 sequence is represented by AAR8744. These muteins contain a non-native cystein residues substituted for one of the first (or last) four amino acid residues of this sequence. Polyethylene glycol (PEG) conjugates are then created from the muteins, where the PEG is attached to the non-native cystein residue. The PEG is attached to the free cystein through an activating group selected from maleimide, cate cystein through an activating group selected from maleimide. The conjugates can also comprise a second polypeptide attached to the PEG. The conjugates may be used for the treatment of IGF associated conditions, such as dwarfism, diabetes, periodontal disease or esteoporosis. Advantages associated with these conjugates are that they have a higher molecular weight, and an extended circulating half life in comparison to wild type IGF.
                                Insulin-like growth factor-1; IGF-1; polyethylene glycol; PEG; triflate; IGF-1/PEG conjugate; maleimide; sulphydryl; thiol; tresylate; aziride; exirane; 5-pyridyl; therapy; dwarfism; diabetes; periodontal disease; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endothelial cell-binding peptide, Genetic display package,
peptide display library, affinity selection, population display package;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conjugates for treatment of, e.g. dwarfism, diabetes, or osteoporosis - comprising polyethylene glycol attached to mutein of IGF at free cysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR95832-R95844 represent the altered fragments of the insulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of an endothelial cell-binding peptide motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 2; I
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 22; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY84999 standard; peptide; 5 AA.
 IGF-1 mutein C67 residues 63-67
                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                95WO-US006540.
                                                                                                                                                                                                                                                                                                                                   94US-00248273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.1%;
                                                                                                                                                                                          /note= "A5C"
                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                     (AMGE-) AMGEN BOULDER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Mcdermott MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-020360/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PLVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PLKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5 AA;
                                                                                                                                                                                                                                                                                                24-MAY-1995;
                                                                                                                                                                                                                                                                                                                                   24-MAY-1994;
                                                                                                                                                                                                                             WO9532003-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-2000
                                                                                                                                                                                                                                                              30-NOV-1995
                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY84999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      Cox GN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY84999
IID AAX8
XX
AC AAX8
XX
DT 21-A
XX
XX
DE Amin
XX
KW Endo
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
The present sequence represents an endothelial cell-binding peptide motif. The peptide may be identified using the method of the invention. The specification describes a method for generating a peptide having a selected biological activity. The method comprises displaying the peptide display library, and using affinity selection to enrich the population display package for those containing peptides which have containing peptides which have desired specificity to the target cell. The method may be used in the deletion of peptides having effects on cell proliferation, differentiation, death and migration, as well as in the identification of peptides which have anti-proliferative activity with respect to one or more types of cells, peptides with (anti-)angiogenic activity, anti-infective peptides (e.g. which are active as anti-fungal or anti-infective peptides (e.g. which are active as anti-fungal or anti-infective peptides (e.g. which are active as anti-fungal or anti-infective no ligand is known. Moreover, the method may be used to test functional ligand-receptor or ligand-ton channel interactions for cell surface-localized receptors and channels
cell proliferation; cell differentiation; cell death; cell migration; angiogenic activity; infective peptide; anti-fungal; anti-bacterial; receptor protein effector.
                                                                                                                                                                                                                                                                                                                                                                         Generating a peptide with a selected biological activity useful for identifying endothelial inhibitors and peptides with anti-anglogenic activity by combining peptide display libraries in a display and a secretion mode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vasotropic; antipsoriatic; dermatological; ophthalmological; antidiabetic; antiarthritic; vulnerary; antiulcer; antiinflammatory; antibacterial; gynaecological; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cell binding protein; ECBP; anti-tumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 3; Length 5;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endothelial cell binding peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 42; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC44308 standard; peptide; 5 AA.
                                                                                                                                                                                     99WO-US024276.
                                                                                                                                                                                                                          98US-00174943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.1%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                  Gyuris J, Morris AJ;
                                                                                                                                                                                                                                                                                                                                      WPI; 2000-339649/29.
                                                                                                                                                                                                                                                               (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :||||
1 IPLVP
                                                                                                              WO200023465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 AA;
                                                                                                                                                                                                                          19-OCT-1998;
                                                                                                                                                                                     19-OCT-1999;
                                                                                                                                               27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC44308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC44308
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

0

ö

Gaps

ö

Length 5;

Tsantrizos Y;

Simoneau B,

```
Score 25, DB 7; Length 5; Pred. No. 1.4e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C; inhibitor; NS3 protease; NS4A cofactor.
                                                                   Morris AJ, Tsaioun K;
                                                                                                                      Claim 3; SEQ ID NO 36; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-Ac-Asp"
                                                                                                                                                                                                                                                                                                                                                        AAY03909 standard, peptide, 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-CA000765
                                                                                                                                                                                                                                                                                48.1%;
80.0%;
                          01-NOV-2002; 2002WO-US035258
                                       01-NOV-2001; 2001US-0334822P
                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                              4; Conservative
                                                     (GPCB-) GPC BIOTECH INC
                                                                   Lamphere L,
                                                                               WPI; 2003-482072/45.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  :||||
1 IPLVP 5
                                                                                                                                                                                                                                                                                                          4 VPLVP
                                                                                                                                                                                                                                                                   Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9907733-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999
             08-MAY-2003
                                                                                                                                                                                                                                                      invention.
                                                                   Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                      AAY03909;
                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                            RESULT 15
                                                                                                                                                                                                                                                                                                                                                   AAY03909
셤
                                                                                                                                                                                                                                                                                                           ð
```

ô

Gaps 0;

```
New generically described peptides are disclosed which are NS3 protease inhibitors useful for treating hepatitis C virus (HCV) infection. The present sequence represents a specific example of these peptides. In a test to determine inhibition in a NS3 protease/NS4A cofactor peptide radiometric assay, this peptide had an ICSO value of 92 micromolar
                                                                                                                                                                                                                                                                                                                                 New peptides inhibitors of NS3 protease - useful for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
46.2%; Score 24; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                Rancourt J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 5, 2004, 11:03:36 Job time : 39.3333 secs
                                                                                               (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 108; 158pp; English.
                                  97US-0055186P
                                                                                                                                                             Poupart M,
                                                                                                                                                                                                                                                                                                                                                               hepatitis C infections.
                                                                                                                                                                                                                                                                WPI; 1999-167361/14.
                                                                                                                                                                Llinas-Brunet M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVPC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6 AA;
                                  11-AUG-1997;
                                                                                                                                                                                                      Wernic D;
      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell binding protein (ECBP) sequences. A peptide of the invention has anticumour, cytostatic, vasotropic, antipsoriatic, dermatological cell tumour, cytostatic, vasotropic, antiarthritic, vulnerary, antiulcer, cantiniflammatory, antidabetic, antiarthritic, vulnerary, antiulcer, cophthalmological, antidabetic, antiarthritic, vulnerary, antiulcer, cophthalmological, cells, by treating, the proliferation and/or migration of endothelial cells, by treating the cells with an ECBP agonist, which is preferably the peptide, to promote proliferation and/or migration of the treated cells, and for reducing or promoting angiogenesis, by treating the cells with an ECBP antagonist, which is also promoting angiogenesis, by treating and medicament for promoting angiogenesis, by admixing an ECBP agonist or ECBP antagonist to promote or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis. ECBP sequences are useful to alter the infectivity spectrum of a viral particle. The present sequence represents an ECBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel synthetic or recombinant polypeptide useful for promoting, reducing proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.
WO2003037172-A2
```

ö

Gaps

; 0

0; Indels Length 6;

```
Sequence 242, App
Sequence 11221, A
Sequence 11221, A
Sequence 11250, A
Sequence 11258, A
Sequence 11259, A
Sequence 11255, A
Sequence 11275, A
Sequence 11275, A
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 2156, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14, Appl
                                                                                                          September 5, 2004, 11:05:54; Search time 35.6667 Seconds (without alignments) 79.502 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                  119143
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-761-636A-14
2 US-10-363-208-242
5 US-10-154-884B-11221
5 US-10-154-884B-11256
5 US-10-154-884B-11256
5 US-10-154-884B-11256
5 US-10-154-884B-11255
5 US-10-154-884B-11255
5 US-10-154-884B-11275
5 US-10-154-884B-11275
6 US-10-154-884B-11275
7 US-10-154-884B-11280
7 US-10-154-884B-11280
7 US-10-363-208-1128
7 US-10-363-208-1128
7 US-10-363-208-1128
7 US-10-363-208-1128
7 US-10-363-208-1128
7 US-10-363-208-1128
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                          1298764 seqs, 315065143 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                      US-09-761-636A-14
52
1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB
Maximum DB
                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š.
```

,		0	c	į.		į
7 T	9 7	0.0	ומ	ς;	-10-395-032-2	
· α		7.0	n d	* 6	-/60-40/-	9 0
0 -	, ,	7.74	n c	0 6	335-52	2.5
) C		7.04	n a	9 6	110 00 000 100 000 100 000 000 000 000	Sequence 439, App
3 6	1 6	7.0	n c	4 -	US-US-352-163-656	9 6
170		7.0	א כ	4 1	US-10-286-457-216	21
77	7 6	۰ و	ורכ		5-10-4	e 30
23	573	44.2	7	י עם	US-09-761-636A-11	11,
24	53	4	σ	0	US-09-997-579-19	19,
25	23	4	Ø.	12	US-10-363-208-147	14
56	23	4	0	12	US-10-363-208-236	236,
27	23	44.2	6	14	US-10-038-407-29	29,
28	23	44.2	6	14	US-10-254-446A-123	123,
29	23	44.2	6	14	55	165
30	23	44.2	6	14	0	200
31	23	44.2	6	14	ும	Semience 15 Appl
32	23	4	0	16	US-10-777-053-304	104
33	22	N	4	o	,	ο
34	22	CA	4	15	US-10-138-375-69	Semience 69 anni
С	22	n	יני	1	287-68	
9 %		10	יו ר	٠ ٥	001/00	0 -
27	, ,	; ,	ר ני	ш	TTC-17-02-75-	Sequence 116, App
000	7 6	٩c	nι	n Ł	13/5-68	9
5 6	77	;	ų,	<u>۲</u>	8-37	9 11
φ.	52		φ	σ	-387-	67,
	52	42.3	<b>9</b>	0	09-947-387-11	115
41	22	42.3	9	14	0-184A-	
42	22	N	y	7	-10-138-375-6	7
43	22		v	, <del>,</del>	-10-138-375-	111
	22	(	7	) o	747-397-	, , , ,
			. [	, -	1	1114, 4
1	1		•	71	C-/TZ-609-0T-	edneuce so
					ALIGNMENTS	
RESULT 1						
US-09-761	-636A-1	14				
; Sequence	14, 1	Sequence 14, Application	ion US/	760,	. US/09761636A	
; Patent 1	to. US:	20020065	218A1			
; GENERAL INFORMATION:	INFOR	MATION:				
; APPLICANT:		CHEN, Ma	ırc			
, APPLICANT:		STACKER, St	Steven			
; APPLICANT:	NT:	HUGHES,	Richard	_		
; APPLIC!	) :EN	CENDRON,	Angela		JANT: CENDRON, Angela	
; TITLE (	F INVE	ENTION:	VEGF-D/	VEG	C/VEGF PEPTIDOMIMETIC	INHIBITOR
; FILE RI	FEREN	FILE REFERENCE: 1064/48505 Achen	/48505	Ach	et al	
; CURRENT	APPLI	CURRENT APPLICATION NUMBER:	=		US/09/761,636A	
CORKEN:	FILL	CURRENT FILING DATE:	2001	01-		
	PPLICE			35	US 60/176,293	
	TLING	FILING DATE: 2		87.		
	PPLICA	APPLICATION NUMBER:			60/204,590	
, PRIOR I	ïr.	FILING DATE: 2000-0	5	-16		
; NUMBER	Œ.	SEQ ID NOS: 34	 4.			
; SOFTWARE	'	centin v	ersion	3.0		
SEQ ID NO	0 14					

0

0; Gaps

100.0%; Score 52; DB 9; Length 9; larity 100.0%; Pred. No. 1.2e+06; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 9; Conserv σ

1 CISVPLVPC ||||||||| 1 CISVPLVPC

임

TYPE: PRT ORGANISM: Homo sapiens

LENGTH:

US-09-761-636A-14

RESULT 2 US-10-363-208-242 ; Sequence 242, Application US/10363208 ; Publication No. US20040048243A1

```
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                |:|||:
CLSVPV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CLSVPV 9
                                                                     1 CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CISVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo s
US-10-154-884B-11228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-154-884B-11250
                                                                                                                                                                                                                                                                                                  US-10-154-884B-11228
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                         ð
                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFFLIANCE CONTINGENTION: Compositions and Methods for the Detection, Diagnosis and Therapy, TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy, TITLE OF INVENTION: Hematological Malignancies
FILE OF INVENTION: Hematological Malignancies
FILE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10.154,884B
CURRENT FILING DATE: 2000-05-23
FRIOR APPLICATION NUMBER: US 60/190,479
FRIOR FILING DATE: 2000-03-17
FRIOR FILING DATE: 2000-03-17
FRIOR FILING DATE: 2000-04-28
FRIOR PAPLICATION NUMBER: US 60/200,779
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-05-01
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING DATE: 2000-06-03
FRIOR FILING 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
GENERAL INFORMATION:
APPLICANT: Board of Regents, The University of Texas System
APPLICANT: Board of Repents, The University of Texas System
TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
FILE REFERENCE: 005774.P005PCT
CURRENT APPLICATION NUMBER: US/10/363,208
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 273
SOFTWARE: Patentin version 3.1
SEQ ID NO 242
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.9%; Score 27; DB 15; Length 9; 66.7%; Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 51.9%; Score 27; DB 12; Length 9; Best Local Similarity 55.6%; Pred. No. 1.2e+06; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide

COATION: (1)..(9)

CTHER INFORMATION: synthetic construct

US-10-363-208-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CMSSPGVAC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-154-884B-11221
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Radiet, Paul A.
APPLICANT: Retter, Marc M.
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Mailgnancies
FILE REPERENCE: 0.046.6.015.2105
FILE OF INVENTION: Hematological Mailgnancies
FILE OF INVENTION: Hematological Mailgnancies
FILE OF INVENTION: WINBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/180,479
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-303
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,99
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
    Indels
    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 15;
Pred. No. 1.2e+06;
2; Mismatches 0
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Sequence 11228, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11250, Application US/10154884B publication No. US20040005561A1 GENERAL INFORMATION:
    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.9%;
```

```
APPLICANT: Manulon, Jane A-
APPLICANT: Manulon, Jane A-
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR PLING DATE: 2000-03-17
PRIOR PLING DATE: 2000-03-17
PRIOR PAPLICATION NUMBER: US 60/200,545
PRIOR PAPLICATION NUMBER: US 60/200,739
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR PLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 15; Le
Pred. No. 1.2e+06;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 15;
Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11258, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
                   PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h
Similarity 66.7%;
4; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Homo sapiens
US-10-154-884B-11254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-154-884B-11258
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CLSVPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CLSVPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -10-154-884B-11258
                                                                                                                                                                                                                                                 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-154-864B-11254
Sequence 11254, Application US/10154884B
Sequence 11254, Application US/10154884B
Sequence 11254, Application US/10154884B
Sequence 11254, Application US.20040005561A1
GENERAL INFORMATION:
JAPPLICANT: Gaiger, Alexander
APPLICANT: March Alexander
APPLICANT: March Alexander
APPLICANT: March Corporation
JTTLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TTLE REFERENCE: 014058-011521US
CURRENT APPLICANTON NUMBER: US/10/154,884B
CURRENT PILING DATE: 2002-05-30
FRICH RELIAND DATE: 2000-03-01
FRICH PILING DATE: 2000-03-01
FRICH PILING DATE: 2000-03-01
FRICH PILING DATE: 2000-04-28
FRICH PILING DATE: 2000-04-28
FRICH PILING DATE: 2000-04-28
FRICH PILING DATE: 2000-04-28
FRICH PILING DATE: 2000-04-28
FRICH PILING DATE: 2000-04-28
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-01
FRICH PILING DATE: 2000-05-04
FRICH PILING DATE: 2000-05-04
FRICH PILING DATE: 2000-05-04
FRICH FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                   CURRENT FILING DATE: 2002-06-23
PRIOR PILING DATE: 2002-06-23
PRIOR PILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-03-17
PRIOR PLILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-28
PRIOR PLILING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-01
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PLILING DATE: 2000-06-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PLILING DATE: 2000-08-03
PRIOR PRILING DATE: 2000-08-03
PRIOR PLILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 15;
Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ORGANISM: Homo sapiens
US-10-154-884B-11250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLSVPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGIH:
```

à g

```
| GRENEAL INCREMATION
| GARGERAL INCREMATION
| APPLICANT: Algate, Paul A. |
| APPLICANT: Algate, Paul A. |
| APPLICANT: Algate, Paul A. |
| APPLICANT: Algate, Paul A. |
| APPLICANT: Manion, Jane A. |
| APPLICANT: Manion, Jane A. |
| APPLICANT: Manion, Jane A. |
| APPLICANT: Retter, Marc W. |
| APPLICANT: Retter, Marc W. |
| APPLICANT: Corixa Corporations and Methods for the Detection, Diagnosis and Therapor ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapor ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapor ITILE OF INVENTION: WORBER: US 60/186,126 |
| PRIOR PILING DATE: 2000-03-17 |
| PRIOR FILING DATE: 2000-03-17 |
| PRIOR FILING DATE: 2000-04-27 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR FILING DATE: 2000-04-28 |
| PRIOR PILING DATE: 2000-05-01 |
| PRIOR FILING DATE: 2000-05-01 |
| PRIOR PILING DATE: 2000-05-01 |
| PRIOR FILING DATE: 2000-05-04 |
| PRIOR FILING DATE: 2000-05-04 |
| PRIOR FILING DATE: 2000-05-04 |
| PRIOR FILING DATE: 2000-05-04 |
| PRIOR FILING DATE: 2000-05-07-14 |
| PRIOR PILING DATE: 2000-07-14 |
| PRIOR PILING DATE: 2000-07-14 |
| PRIOR PILING DATE: 2000-05-14 |
| PRIOR PILING DATE: 2000-07-14 |
| PRIOR PILING DATE: 200
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-005-04
PRIOR PLING DATE: 2000-007-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 27; DB 15;
Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11275, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|||:
CLSVPV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-154-884B-11275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                 APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Marcander
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Marchar Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: MANNER: US 60/186,126
REIGH APPLICATION NUMBER: US 60/180,479
REIGH APPLICATION NUMBER: US 60/180,479
REIGH APPLICATION NUMBER: US 60/200,345
REIGH APPLICATION NUMBER: US 60/200,345
REIGH APPLICATION NUMBER: US 60/200,399
REIGH APPLICATION NUMBER: US 60/200,399
REIGH APPLICATION NUMBER: US 60/200,999
REIGH APPLICATION NUMBER: US 60/222,903
REIGH APPLICATION NUMBER: US 60/222,903
REIGH REILING DATE: 2000-05-01
REIGH APPLICATION NUMBER: US 60/222,903
REIGH REILING DATE: 2000-05-01
REIGH APPLICATION NUMBER: US 60/222,903
REIGH REILING DATE: 2000-05-01
REIGH REILING DATE: 2000-05-01
REIGH REILING DATE: 2000-05-01
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REIGH REILING DATE: 2000-05-03
REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11265, Application US/10154884B

Publication No. US20040005561A1

GENERAL INFORMATION:

APPLICANT: GAIGER, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-0135210S

CURRENT FILING DATE: 2002-05-23

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/200,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels
                                                                                                                   Sequence 11259, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-154-884B-11259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CLSVPV 9
                                                                 -10-154-884B-11259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-154-884B-11265
```

ઠ 셤

٠.

```
FEATURE: OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based OTHER INFORMATION: ability to selectively bind to endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Board of Regents, The University of Texas System TITLE OF INVENTION Methods and Compositions for In Vitro Targeting FILE REFERENCE: 005774, P005PCT CURRENT APPLICATION NUMBER: US/10/363,208 CURRENT PILING DATE: 2003-03-07 NUMBER OF SEQ ID NOS: 273 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: 83P564: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION NUMBER: 60/181,261
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 716
SEQ ID NOS: 716
SEQ ID NO 148
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
TENTING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h Sonatarity 66.7%; Pred. No. 1.2e+06; 4; Conservative 2; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 26; DB 9; I
50.0%; Pred. No. 1.2e+06;
iive 2; Mismatches 2;
                        CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/334822
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 148, Application US/09780053
Patent No. US20020102640A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 137, Application US/10363208; Publication No. US20040048243A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rene S. Hubert
APPLICANT: Daniel B.H. Afar
APPLICANT: Pia M. Challita-Eid
APPLICANT: Mary Paris
APPLICANT: Elana Levin
                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FILE REFERENCE: GPCI-P01-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo Sapiens
US-09-780-053-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SVPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : :|| ||
LPLPLRPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||
AIPLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-09-780-053-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-363-208-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-286-457-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FILE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/10286457
Publication No. US20030166004A1
GENERAL INFORMATION:
APPLICANT: JENO GYURIS et al.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 11290 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%; Score 27; DB 15; Length 9; 66.7%; Pred. No. 1.2e+06;
                                                                                                                                                                                              0; Indels
                                                                                                                            Score 27; DB 15;
Pred. No. 1.2e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE REFERENCE OLGOSE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11280, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
                                                                                                                            51.9%;
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-11280
                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CISVPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|||:
|CLSVPV 9
                                                                                                                                                                                                                                                             CISVPL 6
                                                                                                                                                                                                                                                                                                                           4 CLSVPV 9
                                  ; OKGANISM: DOWN CU
US-10-154-884B-11275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 11280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-10-286-457-21
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
US-10-06-689-2726
US-10-06-689-2726
; Sequence 2726, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blackluk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFRENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT APPLICATION NUMBER: US/11-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PATENTIN VEY. 2.0
                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
CTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-006-869-2726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                      Query Match 50.0%; Score 26; DB 12; Length 9; Best Local Similarity 55.6%; Pred. No. 1.2e+06; Matches 5; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.0%; Score 26; DB 14; Length 9; Best Local Similarity 44.4%; Pred. No. 1.2e+06; Matches 4; Conservative 2; Mismatches 3; Indels
; SEQ ID NO 137
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)...(9)
; CTHER INFORMATION: synthetic construct
US-10-363-208-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                     | |:| | |
1 CRSLPPVRC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2726
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

Search completed: September 5, 2004, 11:16:00 Job time : 35.6667 secs

| :: || | 1 CFALDLVTC 9 1115, App 115, App 116, App 114, App 114, App 114, App 113, App

Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

```
GENERAL INCRMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100066.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2726
LENGTH: 9
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Cyclicized modulating agent comprising OTHER INFORMATION: desmocollin-2 cell adhesion recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1681, Application US/09535852
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 663911
Patent No. 6631
Patent No. 6681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 4; Length 9; Pred. No. 3e+05;
                      US-08-660-092-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2726, Application US/09187859A Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIAFATTPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPLVPC
     US-09-535-852-1681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-187-859-2726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-535-852-1681
     egin{array}{c} egin{array}{c} eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & eta & et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Appliseduence 147, Applisequence 149, Applisequence 150, Applisequence 373, Applisequence 373, Applisequence 19, Applisequence 69, Applisequence 116, Applisequence 68, Applisequence 116, Applisequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Appl
Sequence 147, Appl
Sequence 148, Appl
Sequence 149, Appl
Sequence 150, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1681, Ap
Sequence 2726, Ap
Sequence 2726, Ap
                                                                                                                                                                                                       (without alignments)
38.719 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                        5, 2004, 11:01:38 ; Search time 12 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-535-852-1681

US-09-187-859-2726

US-09-187-859-2726

US-08-189-31-147

US-08-189-31-149

US-08-189-31-149

US-08-189-31-149

US-08-189-31-150

US-08-189-31-150

US-08-171-068-149

US-08-471-068-149

US-08-471-068-149

US-08-471-068-149

US-09-158-759-13

US-09-1579-1373

US-09-042-107-1373

US-09-042-107-1373

US-09-188-69

US-09-188-89

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-521-650-68

US-09-521-650-68

US-09-521-650-116

US-09-521-650-116

US-09-521-650-116

US-09-521-650-116

US-09-168-888-69

US-09-521-650-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Issued Patents AA:*
                                                                                                                                                                                                                                                                              US-09-761-636A-14
52
1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                           September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .........
                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                      Run on:
```

Result No.

. 0

Gaps

0;

```
US-08-189-331-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                 o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS NONCREN PILE REPERENCE: 100086,407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT PILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2726
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: Protocadherin cell adhesion recognition sequence US-09-839-542B-2726
                         FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
CTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: South, Mitichitaka
APPLICANT: Gomi, Komakazu
APPLICANT: Gomi, Komakazu
APPLICANT: Suzuki, Koji
APPLICANT: Suzuki, Koji
APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 26; DB 4; Length 9; ilarity 44.4%; Pred. No. 3e+05; Conservative 2; Mismatcher
                                                                                                                                             Query Match 50.0%; Score 26; DB 4; Length 9; Best Local Similarity 44.4%; Pred. No. 3e+05; Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2726, Application US/09839542B Patent No. 6569996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-261-206A-18
Sequence 18, Application US/08261206A
Patent No. 5574007
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :: || |
1 CFALDLVTC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                 | :: || |
1 CFALDLVTC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                    1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-839-542B-2726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 147, Application US/08189331

Patent No. 574734

GENERAL INFORMATION:
APPLICANT: RAY, B. K.
APPLICANT: ROW, B. K.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NOATH: US/08/189,331
FILING DATE: CONCURRENTly herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 1;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                  FILING DATE:
CLASIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REGISTRATION NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
APPLICATION NUMBER: US/08/261,206A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION POR SEQ ID NO: 147
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%;
                                                                                                                                                                                                                                                       TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                      LECUMNA: 703-2-1-2848
                                                                                                                                                                                                                                                                                                                   : 7 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 amino acids
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-261-206A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                            inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVAPC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-189-331-147
                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
```

.. 0

```
REFERENCE TO THE TOTAL TO THE TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELETEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 150:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
CITY:
CITYE: New 1C.
COUNTRY: U.S.A.
TD: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CVSAP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-189-331-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-08-189-331-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-189-331-149
US-08-189-331-149
Sequence 149, Application US/08189331
Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: Ray, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                            Sequence 148, Application US/08189331
Patent No. 5747334
CENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: FOwlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 1; Length 8; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
44.2%; Score 23; DB 1; Length 8; 60.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATIOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: CONCURTENTLY herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 1101-155
TELEPHONE: 212 790-9090
TELEFRAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.2%;
                                  3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-189-331-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
                 Local Similarity
                                                                     1 CISVP 5
                                                                                                       CVSAP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CVSAP 7
                                                                                                                                                               RESULT 6
US-08-189-331-148
 Query Match
                   Best Loca
Matches
                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 150, Application US/08189331
Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: Kowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.2%; Score 23; DB 1; Length 8; 60.0%; Pred. No. 3e+05; 1; Mismatches 1; Indels
CMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FLING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFRENCHICE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 1101-155
TELEFRANCIS/DOCKET NUMBER: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: CONCURTENTLY herewith
CLASSIFICATION: 435
```

ö

```
US-08-471-068-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAITO, YOSHIMASA
APPLICANT: FUJIMIRA, TARAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
ADDRESSEE: 04
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
SITRET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
SITRET: YIEGHINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                  Score 23; DB 1; Length 8; Pred. No. 3e+05; 1; Indels
                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.2%; Score 23; DB 1; Length 8; 42.9%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: (703) 413-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08633760
Patent No. 5804429
GENERAL INFORMATION:
                                                                                                                                                    44.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 42.93
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           3; Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 amino acids
                                                                           ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-189-331-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIRGINIA
: USA
                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLV 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :||::
CAAVPML 8
                                                                                                                                                                                                                               1 CISVP 5
                                                                                                                                                                                                                                                                   1 ČVŠAP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                          RESULT 9
US-08-633-760-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-633-760-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

RESULT 10

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-471-068-148
) Sequence 148, Application US/08471068
) Fatent No. 5948635
) GENERAL INFORMATION:
APPLICANT: Ray, B. K.
APPLICANT: Ray, B. K.
APPLICANT: Powlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
NUMBER OF SEQUENCES:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                   APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SECURICES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.2%; Score 23; DB 2; Length 8; 60.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pennie & Edmonds STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                             1155 Avenue of the Americas
                                                                                                                                                                                                             STRET: 1155 Avenue of the America CITY: New York STATE: New York COUWTRY: U.S.A. ZIP: 10036-2711 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC COMPALIBLE COMPUTER: 1BM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 147, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMUNICATION INFORMATION:
TELEPRAX: 212 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CVSAP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-471-068-147
```

. 0 us-09-761-636a-14.closed.rai

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                    Sequence 150, Application US/08471068
Patent No. 5948635
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
UNMERS OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.2%; Score 23; DB 2; Length 8; 60.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
FILING DATE:
                                                                                                                                   44.2%; Score 23; DB 2;
60.0%; Pred. No. 3e+05;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: Pennie & Edmonds
1: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,82
REFERENCE/DOCKET NUMBER: 1101-155
TELECHOMUNICATION INFORMATION:
TELECHOMONICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/08891271
; Patent No. 6165476
                                                                                                                                Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                   single
                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-471-068-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                     1 CISVP 5
                                                                                                                                                                                                                                                         2 CVSAP 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                             US-08-471-068-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                       US-08-471-068-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-891-271-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149, Application US/08471068
Patent No. 5948635
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCES ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.2%; Score 23; DB 2; Length 8; 60.0%; Pred. No. 3e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patemitn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
                                                             PILING DAVIE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids

LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 869-8864/9741
TELEFAX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%,
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVSAP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-471-068-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

; 0

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-258-754-373

19-09-258-754-373

2 Sequence 373, Application US/09258754

2 Patent No. 6174687

3 GENERAL INFORMATION:

3 APPLICANT: Ruoslahri, Erkki

3 APPLICANT: Rajotte, Daniel

3 TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using

4 TITLE OF INVENTION: Methods of Dipeptidase

5 TITLE OF INVENTION: Methods of Occupance of Identifying Lung Homing Molecules Using

5 TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using

6 TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using

7 TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using

8 TITLE REFERENCE: P-LJ 3443

9 CURRENT APPLICATION NUMBER: US/09/226

9 EARLIER APPLICATION NUMBER: 09/042,107

10 SEQ ID NOS: 452

11 SEQ ID NO 373

12 LENGTH: 9

13 LENGTH: 9

14 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-373
                  APPLICANT: Strom, Terry B.
APPLICANT: Strom, Terry B.
APPLICANT: Sytkowski, Arthur J.
APPLICANT: Sytkowski, Arthur J.
APPLICANT: Sytkowski, Arthur J.
APPLICANT: Sytkowski, Arthur J.
APPLICANT: Strom, Xin Xiao
TITLE OF INVENTION: Hung Region Linker
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STREET: Usasington
STRTE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIIOM TYPER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PFLIANG DATE: 10-JUL-1997

FLIANG DATE: 10-JUL-1997

CLASSIFICATION NUMBER: 36,361

REGISTRATION NUMBER: 36,361

REGISTRATION NUMBER: 36,361

REFERENCE/DOCKET NUMBER: BH97-07

TELEPAX: 617-861-6240

TELEPAX: 617-861-6240

INPORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acids

TYPE: amino acid

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CISVPLVPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CVECP--PC 8
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-891-271-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
Ouery Match
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PLVPC 9
4 PLVAC 8

Search completed: September 5, 2004, 11:07:05

Job time: 12 secs
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

September Run on:

5, 2004, 09:47:29; Search time 9.9798 Seconds (without alignments) 125.302 Million cell updates/sec

US-09-761-636A-5 72 1 CASELGKSTNTFC 13 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* ..... .....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	ribonuclease-relat	acetate kinase hom	acetate kinase hom	hypothetical prote			membrane-associate	NAC2-like protein	lytB protein [impo	1	pectinesterase (EC	U	protein kinase C (	probable membrane	hypothetical prote	T-cell receptor be	hypothetical prote	hypothetical prote	ng	probable RNA helic	$\Xi$		probable allene ox	probable alpha-tre	hypothetical prote	MG243 homolog H91	qermin homolog F21	viral capsid prote	ORF MSV185 hypothe
	ID	A39035	57	AH1220	T17722	S42384	C85018	G97177	623	A84947	S53818	S70914	835362	T43051	877690	809778	B49046	134	17	834421	H71410	837055	S44780	A71419	T41711	6907	32	T01199	JC6158	4
	DB 1	1																			2	3 2							7 2	
	Length	104	397	397	383	409	1117	378	469	318	421	433	386	1174	1294	23(	35	282	372	416	442	48	683	$\vdash$	947	3	224	9	4	9
*	Query Match	59.7	56.9			54.2			52.8	51.4	51.4	51.4	51.4	51.4	51.4	50.7	50.0	50.0	50.0	50.0	50.0	50.0	20.0	50.0				•	48.6	•
	Score	i	41	41	40	39	39	38	38	37	37	37	37	37							36							5	35	
	Result No.		7	3	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17			20									29

toxin CssII - Mexi	cdu3 protein - Clo	conserved hypothet	hypothetical prote	probable lipoprote	hypothetical prote	hypothetical prote	inner cell wall ma	hypothetical prote	hypothetical prote	hypothetical prote	alanine racemase,	acetate kinase (EC	acetate kinase (EC	competence-damage	protein kinase (EC
A27406	PC4272	D82152	H71899	AF0199	T33545	867199	877699	AF2007	S27641	AF1990	H82329	E64239	D81339	A11611	T43234
N	N	Ŋ	N	N	N	7	(7)	N	N	~	7	7	0	~	Н
99	80	155	182	207	218	228	238	265	276	308	375	393	396	415	483
48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6
35	35	32	35	35	32	32	35	35	35	35	35	35	35	35	35
0	<u>.</u>	32	33	14	55	99	3.7	38	39	0	11	7	ij	14	ιÖ

## ALIGNMENTS

_		
111	335	

Cibecies: Rana pipiens (northern leopard frog)
Cispecies: Albi-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
Ciscession: Al9035
Riadelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl A;Reference number: Al9035; MUID:91093131; PMID:1985896
A;Reference number: Al9035
A;Reference number: Al9035
A;Reference number: Al9035
C;Superfamily: pancreatic ribonuclease

Gaps 0; 59.7%; Score 43; DB 2; Length 104; llarity 61.5%; Pred. No. 1.7; Conservative 1; Mismatches 4; Indels 4; Query Match Best Local Similarity Matches 8; Conserv

ö

1 CASELGKSTNTFC 13 ò

CKYKLKKSTNKFC 87 q

acetate kinase homolog AckA2 [imported] - Listeria innocua (strain Clip11262)

Accession: Action Manager Montage action of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of

PIDN:CAC96363.1; PID:g16413591; GSPDB:GN00178

A, Residues: 1-397 (GLA)>
A, Residues: 1-397 (GLA)>
A, Cross-references: GB: ALS92022; PIDN: C)
A, Experimental source: strain Clip11262
C, Genetics:

A,Gene: AckA2 C,Superfamily: acetate kinase

Gaps .,0 Query Match 56.9%; Score 41; DB 2; Length 397; Best Local Similarity 72.7%; Pred. No. 14; Matches 8; Conservative 0; Mismatches 3; Indels

ö

0,

Gaps

· 0

2; Length 409; Indels

```
submitted to the EMBL Data Library, March 1994
A;Reference number: $42368
A;Accession: $42384
A;Accession: preliminary
A;Molecule typeliminary
A;Residues: 1-409 <SMI>A;Cross-references: EMBL:Z30662; NID:g459581; PID:g459587
                                                                                                                                                                                                                             Score 39; DB 2
Pred. No. 33;
1; Mismatches
                                                                                                                                                                                   A; Introns: 10/3; 48/3; 182/3; 315/3; 360/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.2%;
58.3%;
                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                             229 CKSDLGSPTQTF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               922 CLSELGELSSTF 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                   1 CASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1117 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-378 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: G97177
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Gene: AT4g01400
A, Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: CAC2253
                                                                                                                                                                C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                  Figlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Status: preliminary
A Molecule type: DNA
A;Residues: 1-397 <GLA>
A;Cross-references: GB:NC_002210; PIDN:CAC99246.1; PID:g16410584; GSPDB:GN00177
A;Experimental source: strain EGD-e
                                                                                                                                                                                 acetate kinase homolog AckA2 [imported] - Listeria monocytogenes (strain EGD-e) C.Species: Listeria monocytogenes (C.Species: Listeria monocytogenes (C.Spate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C.Accession: AH1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein A231L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Accession: T17722
R;Graves, M.V.; Van Etten, J.L.
Rsprinted to the EMBL Data Library, May 1999
A;Reference number: Z18806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kruppel-like protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Cct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
C;Accession: S42384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.9%; Score 41; DB 2; Length 397; Best Local Similarity 72.7%; Pred. No. 14; Matches 8; Conservative 0; Mismatches 3: Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-383 <GRA>
A;Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96599.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 2;
Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 CVMNIGKKKNEFC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: acetate kinase
                                                                     214 CAIEAGKSVNT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 CAIEAGKSVNT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGKSTNT 11
                         CASELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: AckA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: A231L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                           ò
                                                                   g
```

```
membrane-associated sensory histidine kinase-like ATPase [imported] - Clostridium acetok
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001
C;Date: 14-Sep-2001

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
A; Cross-references: GB:NC_001268; NID: 97267637; PIDN: CAB80949.1; GSPDB: GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001437; PIDN:AAK80210.1; PID:g15025255; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 2; Length 1117;
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%; Score 38; DB 2; Length 378; 63.6%; Pred. No. 47; cive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6.
The Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CASELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

C; Accession R; Smith, A.

ò

Gaps

```
C;Accession: S70914; S70913

C;Accession: S70914; S70913

R;Shevchik, V.E.; Condemine, G.; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.

submitted to the EMBL Data Library, February 1995

A;Description: Characterization of pectin methylesterase B, an outer membrane lipoprotei
A;Reference number: S70914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-433 < GRES.
A; Residues: 1-433 < GRES.
A; Cross-references: EMBL: K84665; NID: 91212890; PIDN: CAA59151.1; PID: 91212891
A; Cross-references: EMBL: G; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.
R; Shevchik, V.E.; Condemine, G; Hugouvieux-Cotte-Pattat, N.; Robert-Baudouy, J.
A). Michobiol. 19, 455-466, 1996
A; Title: Characterization of pectin methylesterase B, an outer membrane lipoprotein of EA; Reference number: S70913; MUID: 96228695; PMID: 88330237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase C (EC 2.7.1.-) pckl - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: pombe C-kinase 1
N;Alternate names: pombe C-kinase 1
C;Speciess Schizosaccharomyces pombe
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 06-Oct-2000
C;Accession: S35362; T37866; T38203
M; Yanda, T.; Shimanuki, M.; Yanagida, M.
EMBO J. 12, 1987-1995, 1993
A;Title: Two novel protein kinase C-related genes of fission yeast are essential for cel
A;Reference number: S35362; MUID:93259141; PMID:8491190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pectinesterase (BC 3.1.1.11) precursor - Brwinia chrysanthemi
NiAlternate names: pectin methylesterase
CiSpecies: Erwinia chrysanthemi
CiSpecies: 28-0cr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:D14337; NID:g303938; PIDN:BAA03267.1; PID:g303939 R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-421 <SUU>
A;Cross-references: GB:U10185; NID:g595379; PIDN:AAA82179.1; PID:g595380
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
A;Moleoule type: DNA
A;Residues: 1-53;234-361 <SHA>
A;Cross-references: EMBL:X84665; NID:g1212890; PIDN:CAA59151.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: carboxylic ester hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-433/Product: pectinesterase #status predicted <MAT>
                                                                                                                                                      Score 37; DB 2;
Pred. No. 79;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB
Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain 3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: pectinesterase pemB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%;
                                                                                                                                                         h 51.4%;
Similarity 54.5%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:: | : || |
192 CATKAGATINTTC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 46.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                     1 CASELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                            CSGSLGKTANT 23
                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-988 <TOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S70914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S70913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Start codon: GTG
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q
                                                                                                              T46230

NAC2-like protein - Arabidopsis thaliana

NAC2-like protein - Arabidopsis thaliana

NAC2-like protein - Arabidopsis thaliana (mouse-ear cress)

C; Species: Arabidopsis thaliana (mouse-ear cress)

C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C; Accession: T46230

R; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999

A; Reference number: Z23026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
$53818
XPMC2 protein - African clawed frog
XPMC2 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000
C;Accession: S53818
R;Su, Jv. Maller, J.L.
Mol. Gen. Genet. 246, 387-396, 1995
A;Title: Cloning and expression of a Xenopus gene that prevents mitotic catastrophe in A;Reference number: S53818; MUID:95157530; PMID:7854324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyte protein [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: A84947
R;Shigenobu, S:; Watenabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
A;Reference number: A84930; MUID:20445173; PMID:10993077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.4%; Score 37; DB 2; Length 319; Best Local Similarity 70.0%; Pred. No. 61; Matches 7; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL132964
A;Experimental source: cultivar Columbia; BAC clone T9C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 2;
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STC>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: penicillin tolerance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 3
A;Introns: 60/1; 153/3; 233/3; 332/3; 402/3
A;Note: T9C5.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.8%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
278 CASDIEKSTIT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 SELGSSYNTF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 AĔĽĠKEŤGŤF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-469 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: T46230
A,Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S53818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: lytB; BU147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics:
a
```

q

à

ð

; 0

Gaps

```
ANOLES YOL075C
C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C; Superfamily: unassigned ATP-binding; P-loop; transmembrane protein
C; Superfamily: unassigned ATP-binding; P-loop; transmembrane protein
C; Keywords: ATP; nucleotide binding; P-loop; transmembrane protein
F; 52-63/Domain: ATP-binding cassette homology <ABCl.>
F; 52-69/Region: nucleotide-binding motif A (P-loop)
F; 376-392/Domain: transmembrane #status predicted <TM2>
F; 466-485/Domain: transmembrane #status predicted <TM3>
F; 666-622/Domain: transmembrane #status predicted <TM5>
F; 710-916/Domain: ATP-binding motif A (P-loop)
F; 710-114/Domain: transmembrane #status predicted <TM5>
F; 1125-114/Domain: transmembrane #status predicted <TM6>
F; 1125-1193/Domain: transmembrane #status predicted <TM6>
F; 1117-1193/Domain: transmembrane #status predicted <TM6>
F; 1125-1285/Domain: transmembrane #status predicted <TM7>
F; 11269-1285/Domain: transmembrane #status predicted <TM7>
F; 11269-1285/Domain: transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Systyme to the protein ULI6 precursor - human cytomegalovirus (strain AD169)
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S09778
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.;
M.; Barrell, B.G.
Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegaloviru
A;Accession: S09778
A;Accession: S09779
A;Accession: S09779
A;Accession: S09779
A;Reference number: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUD:90269039; PMID:2161319
A;Accession: B09778
A;Reference subservation acquence hot shown; translation not shown
A;Redidues: 1-230 cCHE>
A;Reaidues: 1-230 cCHE>
A;Reaidues: BMBL:X17403; NID:955591; PIDN:CAA35448.1; PID:955620
A;Coss-references: BMBL:X17403; NID:955991; Data Library, December 1989
C;Superfamily: human cytomegalovirus hypothetical protein Uli6
C;Reywords: glycoprotein; transmembrane protein
F;125-230/Product: hypothetical protein Uli6 #status predicted cMMT>
F;189-206/Domain: signal sequence #status predicted cMM>
F;189-206/Domain: transmembrane #status predicted cTMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
R;Alexandraki, D.; Katsoulou, C.; Tzermia, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66756
A;Recession: 377690
A;Molecule type: DNA
A;Residues: 1-1294 <ALE>
A;Cross-references: EMBL:Z74316; MIPS:YOL075c
A;Note: this is a revision to the sequence from reference S66756
A;Accession: S66767
A;Accession: S66767
A;Accession: S66767
A;Accession: S66767
A;Residues: 1-179: UNA
A;Residues: 1-179: UNA
A;Residues: 1-179: UNA
A;Residues: 1-179: UNA
A;Residues: 1-179: UNA
A;Residues: 200-1294 <ALF>
A;Cross-references: EMBL:Z74817
A;Residues: 200-1294 <ALF>
A;Cross-references: EMBL:Z74817
A;Residues: 200-1294 <ALF>
A;Cross-references: EMBL:Z74817
A;Residues: 200-1294 <ALF>
A;Cross-references: EMBL:Z74817
A;Residues: 200-1294 <ALF>
A;Cross-references: A;Cross-reference of protein YOL075c
C;Genetics:
A;Cross-references: SGD:S0005435
A;And postition: 15L
A;Note: this was assumed to be the complete sequence of protein YOL075c
C;Genetics:
A;Cross-references: SGD:S0005435
A;Note: vinforc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 2; Length 129
Pred. No. 2.3e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1161 CGERLGIMTNTF 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Introns: 767/2; 834/3; 897/3; 959/1
Superfamily: yeast protein kinase C zinc-binding repeat homology; pr C;Superfamily: yeast protein kinase C; protein kinase C zinc-binding; phosphotransferase; serine/threonine F;414-461/Domain: protein kinase C zinc-binding repeat homology <KZ1> F;481-530/Domain: protein kinase C zinc-binding repeat homology <KZ2> F;662-923/Domain: protein kinase C zinc-binding repeat homology <KZ2> F;662-923/Domain: protein kinase Annology <KIN> F;667-678/Region: protein kinase Annology okina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 146/1; 234/1; 559/1; 952/2; 1019/3; 1155/1
C;Superfamily: yeast protein kinase C; protein kinase C zinc-binding repeat homology; pr
C;Kywords: ATP; phospholipid binding; phosphotransferase; serine/threonine-specific pro
F;459-506/Domain: protein kinase C zinc-binding repeat homology «KZNI»
F;527-576/Domain: protein kinase C zinc-binding repeat homology «KZNI»
                                                                                                                                                                                                                               Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEMS Microbiol. Lett. 165, 273-280, 1998
A;Title: PKC1, encoding a protein kinase C, and FAT1, encoding a fatty acid transporter
A;Reference number: Z22303; MUID:98415124; PMID:9742699
A;Accession: T43051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein YOL075c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O1125; hypothetical protein O1130; hypothetical
C;Species: Saccharomyces cerevisiae
C;Date: 21-Apr-1997 #sequence revision 09-May-1997 #text_change 19-Apr-2002
C;Accession: S77690; S66767; $66768
                                                                                                                                           A;Residues: 93-988 <DEV>
A;Residues: 93-988 <BEV>
A;Cross-references: RMBL:Z69795; PIDN:CAA93697.1; GSPDB:GN00066; SPDB:SPAC17G8.14c
B;Grishchuk, K.; McIntosh, J.R.; Devlin, K.; Churcher, C.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, Rebruary 1996
                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-26,'ANVASTKNP',36-137 <GRI>
A;Residues: 1-26,'ANVASTKNP',36-137 <GRI>
A;Cross-references: BMBL:Z69730; PIDN:CAA93602.1; GSPDB:GN00066; SPDB:SPAC22H10.01c
A;Experimental source: strain 972h-; cosmid c22H10
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1174 <052
A;Residues: 1-1174 <052
A;Cross-references: EMBL:Y15839; NID:g2687848; PIDN:CAA75801.1; PID:g2687849
A;Experimental source: strain C2 (ATCC 48329)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase C (EC 2.7.1.-) PKC1 - fungus (Cochliobolus heterostrophus)
C;Species: Cochliobolus heterostrophus, Bipolaris maydis
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.4%; Score 37; DB 2; Length 1174;
46.7%; Pred. No. 2.1e+02;
ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1; I
Pred. No. 1.8e+02;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   996 CKEEMWYGSTTSTFC 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASEL--GKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGNTTSTFC 825
                                                                                                                                                                                                                                                                                                      A; Reference number: Z21778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7; Conserv
                                                                                                               Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: T43051
Oeser, B.M.
                                                                       Accession: T37866
                                                                                                                                                                                                                                                                                                                                          A; Accession: T38203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: pck1
A; Map position: 1L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: pkc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       877690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           දි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

F;35,41,68,84,95,101,132,145/Binding site: carbohydrate (Asn) (covalent) #status predict

1; 1; Gaps Query Match
50.7%; Score 36.5; DB 2; Length 230;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 8; Conservative 3; Mismatches 2; Indels 1

1 CASELG-KSTNTFC 13 || :|| || :|| || 25 CAVDLGSKSSNSTC 38

Search completed: September 5, 2004, 10:01:14 Job time : 11.9798 secs

Dp ð

This Page Blank (uspto)

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

September 5, 2004, 09:38:39; Search time 5.90909 Seconds (without alignments) 114.554 Million cell updates/sec Run on:

US-09-761-636A-5 72 Title: Perfect score: Sequence:

1 CASELGKSTNTFC 13

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	915 homo sap	rattı	mus a		liste	Q8y7v1 listeria mo	P34568 caenorhabdi			homo sa	Q47474 erwinia chr		-	Q08234 saccharomyc	٠.		P34352 caenorhabdi	P33569 streptomyce			Q9ptd7 xenopus lae		P56715 homo sapien	P08900 centruroide	_	_	Q9kuy6 vibrio chol		Q9pp18 campylobact	89aq0 ]	24082		P03378 human immun
SUMMARIES	ID		VEGD RAT	VEGD MOUSE		ACK2_LISIN	ACK2_LISMO	YNV5 CABEL		ISPH BUCAI				KPC1_COCHE	YOHS YEAST	UL16 HCMVA	PPNK HALN1	YK86_CAEEL	BCA STRVL	ESR2 MICUN	TPSX_SCHPO	CING_XENLA	Y243 MYCPN	RP1_HUMAN	SCX2_CENSU	CW14_YEAST	ISPH BUCAP	ALR1 VIBCH	ACKA MYCGE			TRAN_ECOLI	PARC_RHIME	ENV_HV1A2
	DB	7	Н	Н	Н	Н	ч	٦	٦	-	Н	-	Н	-	~	-	Н	Н	Н	Н	Н	-	•	Н	• •		•		•			Н		
	Length	. ~	326	358	104	397		451	9	319	0	433	988	1174	1294	230	282	362	483	673	944	1360	224	2156	99	238	313	361	393	396	576	602	758	855
d	ᅩ드	5.	70.8	70.8	59.7	56.9	56.9	54.2	51.4	51.4	51.4	51.4	51.4	51.4	51.4	50.7	50.0	50.0	50.0	50.0	50.0	50.0	49.3	49.3	48.6	48.6	48.6	48.6	48.6	48.6	•	80	48.6	48.6
	Score	1	51	51	43	41	41	39	37	37	37	37	37	37	37	36.5	36	36	36	36	36	'n	35.5	'n,	35	35	35	35	35	35	35	35	35	35
	Result No.	:	7	e	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

009349 caenorhabdi 013356 cryptococcu P24583 saccharowyc P09811 escherichia 060014 kluyverowyc Q91250 saccharowyc Q1252 saccharowyc P32572 saccharowyc O31605 bacillus su P57628 huchhera an	029100 sus scrofa 091574 xenopus lae
UBEA CAEEL CHS1_CRYNE KPC1_YEAST GLTB_ECOLI UBRA_KLULA BPA1_MOUSE BPA1_MOUSE SP18_YEAST SP18_YEAST SP18_YEAST SP18_YEAST SP18_YEAST SP18_YEAST SP18_YEAST	UPTI_PIG CRT1_XENLA
аананана	
980 1041 1151 1517 1941 7389 245 300 609	122 335
6666666999	200
44444444 8888 666 666 666 666 666 666 66	47
	3.4 4.4 4.4
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 7 4 0

## ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon, and pancreas.

The complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. First form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; P800249; PDGF 1; 1.
PROSITE; P800249; PDGF 2; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat; Cleavage on pair of basic residues; Multigene family.
SIGNAL 1 21 POTENTIAL.
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                    MEDLINE=20011413; PubMed=10542248;
Stacker S.A., Stenvers K.L., Caesar C., Vitali A., Domagala T.,
Nice E.C., Roufail S., Simpson R.J., Moritz R., Karpanen T.,
                                                                                                                                                                                                  'Biosynthesis of vascular endothelial growth factor-D involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the PDGF/VEGF growth factor family.
                                                                                                                        PROCESSING, AND SEQUENCE OF 89-94; 100-105 AND 206-213.
                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Y12864; CAA73371.1; -
EMBL; Y12865; CAA73371.1; JOINED.
EMBL; Y12867; CAA73371.1; JOINED.
EMBL; Y12868; CAA73371.1; JOINED.
EMBL; Y12869; CAA73371.1; JOINED.
EMBL; Y12870; CAA73371.1; JOINED.
EMBL; Y12870; CAA73371.1; JOINED.
EMBL; ADOUGUSS; CAA73371.1; JOINED.
EMBL; ADOUGUSS; CAA73371.1; -
HSSP; P15692; LVPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D89630; BAA24264.1; -. EMBL; Y12863; CAA73370.1; -.
                                                                                                                                                                                    Alitalo K., Achen M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P15692; 1VPP.
Genew; HGNC:3708; FIGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00141; PDGF
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
           á
OR 99 (IN A MINOR FORM).
VASCULAR ENDOTHELIAL GROWTH FACTOR
                             4 X 16 AA REPEATS OF C-X(10) -C-X-C-
                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                              .,
                                                                                                                                                                                          Score 54; DB 1; Length 354; Pred. No. 0.018;
                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                             0; Indels
                                                                                                                                                             N-LINKED (GLCNAC. . .) (PC 2048D769D735173E CRC64;
                                       X(1,3)-C.
1 (APPROXIMATE).
                                                                                                                                                                                                 100.0%; Preu.
                                                                                                                                                                                                                                                                                                       326 AA
                                                                                                                                                                        40444 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF014827; AAB66557.1; -.
                                                                                                                                                                                          75.0%;
                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                    121 ASELGKSTNTF 131
                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                 2 ASELGKSTNTF 12
 88
205
354
318
                                                                    293
318
153
189
1191
1145
1145
1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Sprague-Dawley;
                                                                                       111
142
146
136
155
185
287
354 AA;
                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                            FIGF OR VEGFD
                                                                                                            DISULFID
                                                                                        DISULFID
                                                                                                                                          CARBOHYD
                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                       VEGD RAT
                                                                                                   DISULFID
                                                                                                                                DISULFID
                                                                                                                                                              CARBOHYD
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                          Query Match
                            DOMAIN
                     PROPEP
                                                 REPEAT
                                                            REPEAT
                                                                    REPEAT
                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                035251
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                  RESULT 2
VEGD RAT
 à
```

```
CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annoration update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced growth factor) (FIGF).
FIGF OR VEGFD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
         InterPro; IPR004153; CXCXC repeat.
InterPro; IPR000072; PD growth_factor.
Pfam; PF00141; PDGF: 1.
ProDom; PD001629; PD growth_factor; 1.
ProDom; PR00141; PDGF: 1.
PROSITE; PS00249; PDGF: 1.
PROSITE; PS00249; PDGF 2; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CSTBL/6J; TISSUE=Fibroblast,
MEDLINE=97030224; PubMed=8876195;
MCDiandini M., Marconcini L., Ferruzzi R., Oliviero S.;
"Identification of a c-fos-induced gene that is related to the platelet-derived growth factor/vascular endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                      4 (INCOMPLETE).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY CANCO...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada Y., Nezu J.-I., Shimane M., Hirata Y.;
"Molecular cloning of a novel vascular endothelial growth factor,
VEGF-D.";
                                                                                                                                                                                                                               VASCULAR ENDOTHELIAL GROWTH FACTOR
                                                                                                                                                                                                                                                  POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
1 (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 1; Length 326; Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1261AFA373596C00 CRC64;
                                                                                                                                                                           Cleavage on pair of basic residues; Multigene family SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 93:11675-11680(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97349118; PubMed=9205122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 42:483-488(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.9
ses 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 ASELGKTTNTF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 AA;
HSSP; P15692; 1VPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IISSUE=Lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGD MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                               CHAIN
PROPEP
DOMAIN
                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                              PROPEP
                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eamily
                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SO THE FITTE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
```

```
Manipure sesselo perfect of the marine figg gene, a grooth factor belonging to place for two following to place for two discours of the marine figg gene, a grooth factor family.

Manipurging expression pattern of the marine figg gene, a grooth factor belonging to place for two discours for the factor family.

Men. Per. 7:221-224 (1998).

Men. Per. 7:221-224 (1998).

Men. Per. 7:221-224 (1998).

Men. Per. 7:221-224 (1998).

Men. Per. 13 different in mouse and man. 3.

Men. Per. 13 different in mouse and man. 3.

Men. Per. 13 different in mouse and man. 3.

Men. Per. 13 different in mouse and man. 3.

Men. Per. 13 different in mouse and man. 3.

Men. Per. 14 different in mouse and man. 3.

Men. Per. 14 different in mouse and man. 3.

Men. Per. 15 different in mouse and man. 3.

Men. Per. 15 different in mouse and man. 3.

Men. Per. 15 different in mouse and man. 3.

Men. Per. 15 different in mouse and man. 3.

Men. Per. 15 different in mouse and man. 3.

Men. Per. 15 different in mouse felcts on the permedial prowed in maintenance of differentiated lymphatic emborates, and adles in the maintenance of differentiated lymphatic emborates, and adles in the maintenance of differentiated lymphatic emborates, and adles in the maintenance of differentiated lymphatic emborates, and adles in the maintenance of differentiated lymphatic emborates, and adles in the maintenance of differentiated lymphatic emborates, and adles in the maintenance of differentiated lymphatic emborates, and maintenance of differentiated lymphatic emborates, and maintenance of differentiated lymphatic emborates, and maintenance of different manipulation which generates a content by demains of the mouse of the prof. 70 dema. 3 demails (MPB)

Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 Men. 15 M
```

```
ACK2 LISIN
           ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                    SEQUENCE
                                                           HELIX
STRAND
HELIX
                                                                                                            STRAND
HELIX
                                                                                                                                                                               STRAND
                                                                                                                                                                                                                                                                                                                                                           292CN9;
                                                                                                                                                   STRAND
                                                                                                                                                             STRAND
                                                                                                                                                                                                            STRAND
                                                                                                                                HELIX
                                                                                                                                                                                                                                                                                                                                         ACK2_LISIN
                                                                                        TURN
                                                                                                   TURN
                                                                                                                                           TURN
                                                                                                                                                                       TURN
                                                                                                                                                                                                                                                                                                                                RESULT 5
   g
                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                              ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mosimann S.C., Ardelt W., James M.N.G.;
"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";
J. Mol. Biol. 236:1141-1153 (1994).
-1- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative molecular modeling and crystallization of P-30 protein:
3.

BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo;
MEDLINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniáta, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana,
NCBI_TaxID=8404,
                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93066156; PubMed=1438177;
Mosiman S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                 Score 51; DB 1; Length 358;
Pred. No. 0.066;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRROLIDONE CARBOXYLIC ACID.
                                                                                                 6636B17FBF07037C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; 3D-structure;
Pyrrolidone carboxylic acid.
MOD RES 10 PYRROLIDONE CARBOXYL
ACT_SITE 10
                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29.0 protein (EC 3.1.27.-) (Onconase).
Rana pipiens (Northern leopard frog).
                                                                                                                                                                                                                              104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=94166079; PubMed=8120892;
                                                                                                 М.
                                                                                                                    70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
                                                                                                                              90.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embryos.";
Proteins 14:392-400(1992).
                                                                                                                              Local Similarity 90.9
1es 10; Conservative
                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                            126 ASELGKTTNTF 136
                                                                                                                                                          2 ASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE MODELING.
                                     151
141
150
160
190
292
358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                James M.N.G.;
                                                                                                                                                                                                                            RN30 RANPI
P22069;
        REPEAT
DISULFID
DISULFID
                                                                  CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                DISULFID
                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                      DISULFID
 REPEAT
                                                                                                                                                                                                                RN30_RANPI
                                                                                                                                      Matches
                                                                                                                                                                                                         RESULT 4
FT
FT
FT
FT
SO
SO
SO
                                                                                                                                                          ð
                                                                                                                                                                            엄
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ÷.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claser P., Frangel L., Buchrieser C., Rusnick C., Amend A.,
Charbit A., Checuani E., Buchrieser C., Rusnick P., Chakraborty T.,
Charbit A., Checuani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Sinnes N., Tierrez A.,
"Comparative genomics of Listeria species."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ATP + acctate = ADP + acctyl phosphate. PATHWAY: Conversion of acctate to acctyl-CoA; first step. SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.7%; Score 43; DB 1; Length 104; 61.5%; Pred. No. 0.57; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listeria innocua.
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                  11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Belongs to the acetokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetate kinase 2 (EC 2.7.2.1) (Acetokinase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               397 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 CKYKLKKSTNKFC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACKA2 OR LIN1132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1642;
```

```
·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21537279; Pubmd=11679669;
A Glaser P. Frangeul L. Buchrieser C., Rusniok C., Amend A.,
A Glaser P. Brangeul L. Buchrieser C., Rusniok C., Amend A.,
Baquero P., Berche P., Elocker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
Domann E., Dominquez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Brian K.-D., Fshih H., Garcia-del Portlilo P., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf JO, P.,
Andueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Varquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
Comparative genomics of Listeria species.";
Science 294:89-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: ATP + acetate = ADP + acetyl phosphate.
-!- PATHWAY: Conversion of acetate to acetyl-CoA; first step.
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the acetokinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%; Score 41; DB 1; Length 397; 72.7%; Pred. No. 5.2; 1.1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                      Pram; PRO0871; Acetate Kinase; 1.
PRINTS; PR00471; ACETAȚEKNASE.
TIGRFAMS; TIGR0016; ACETAȚE KINASE.
PROSITE; PS01075; ACETATE KINASE.1; 1.
PROSITE; PS01076; ACETATE KINASE.2; 1.
Transferase; Kinase; Complete proteome.
SEQUENCE 397 AA; 43115 MW; 5822544EF92CBF51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acetate kinase 2 (EC 2.7.2.1) (Acetokinase 2)
   send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                            ListiList, LIN01132; -.
MAMAP; MR 00020; -; 1.
IIILEPPRO; IPR000890; Acetate_kin.
InterPro; IPR004372; AckA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ListiList, LM001168; -.
MAMAP, WF 00020; -; 1.
InterPro; IPR000890; Acetate_kin.
InterPro; IPR004372; AckA.
                                                              EMBL; AL596167; CAC96363.1; -. PIR; AC1574; AC1574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL591978; CAC99246.1; -. PIR; AH1220; AH1220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=EGD-e / Serovar 1/2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 CAIEAGKSVNT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CASELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetate kinase 2
ACKA2 OR LMO1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACK2 LIS
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DD
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                       DB 1; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.2%; Score 39; DB 1; Length 451; 58.3%; Pred. No. 14; ive 1; Mismatches 4; Indels
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Durbin R.; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                         6E295A59A5FD5C5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B36B1C618FBBB3A3 CRC64;
                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein T16H12.5 in chromosome III.
                                                                                                                   56.9%; Score 41; DB 1
72.7%; Pred. No. 5.2;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                        451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 MATH domain.
-!- SIMILARITY: Contains 1 BTB/POZ domain.
         PRINTS, PRO0471; ACETATEKNASE,
TIGRFAMS; TIGRO0016; acka; 1.
PROSITE; PS01075; ACETATE KINASE 1; 1.
PROSITE; PS01076; ACETATE KINASE 2; 1.
Transferase; Kinase; Complete proteome.
SEQUENCE 397 AA; 43132 MW; 6E295A55
 Pfam; PF00871; Acetate_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000210; BTB_POZ.
InterPro; IPR002083; MATH.
InterPro; IPR008914, Traf_dom.
Pfam; PF00921; BTB; 1.
SMART; SM000225; BTB; 1.
SMART; SM00061; MATH; 1.
                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51062 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z30662; CAA83138.2; -. WormPep; T16H12.5; CE29054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS50097; BTB; 1.
PROSITE; PS50144; MATH; 1.
Hypothetical protein.
                                                                                                                Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:|| | ||
271 CKSDLGSPTQTF 282
                                                                                                                                                                                                             214 CAIEAGKSVNT 224
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CASELGKSTNTF 12
                                                                                                                                                                               1 CASELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                                                              T16H12.5.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Bristol N2; Smith A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                      CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                   P34568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                     YNV5_CAEEL
                                                                                                                                                                                                                                                                                      YNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                         RESULT 7
% ¥ B B B B B B
                                                                                                                                                                                 ठे
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
```

```
605542;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ISPH_BUCAI
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20318623; PubMed=10860666;

MEDLINE=20318623; PubMed=10860666;

Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,

Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smutko J.S.,

Zhou H., Leiby K.R., Holmgren L.W., Gearing D.P., Pan Y.;

Zhou H., Leiby K.R., Holmgren L.W., Gearing D.P., Pan Y.;

The transport of the organization of three novel members of the composition of the organization of three novel members of the composition of the composition of the composition of an independent signaling system analogous to interleukin-1 alpha (IL-1A), beta (IL-1B) receptor agonist and interleukin-1 and takes part in local inflammatory response.

C. -- TISSUE SPECIFICITY: Highly expressed in tissues containing epithelial cells: skin, lung, stomach and esophagus. In skin is endothelial cells skin, lung, stomach and esophagus. In skin is endothelial sells of melanocytes. Up-regulated in lesional processed in the containing epithelial cells of melanocytes. Up-regulated in lesional contains the containing epithelial sells of melanocytes. Up-regulated in lesional contains the containing epithelial sells of melanocytes. Up-regulated in lesional contains the containing epithelial sells of the containing epithelial cells of the containing epithel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ragner J., Edwards G., Clifford T., Menon S., Bazan J.R., Lo S.,
Kaetelein R.A.;
"Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function
as an antagonist and agonist of NF-kappa B activation through the
orphan IL-1 receptor-related protein 2.";
J. Immunol. 167:1440-1446(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and initial characterization of four novel members of
                                                                                                                                           28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin 1 family member 9 (IL-1F9) (Interleukin-1 homolog 1) (IL-1H1) (Interleukin-1 epsilon) (IL-1 epsilon) (IL-1 related protein 2)
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Keratinocytes;
MEDLINE=20209405; PubMed=10744718;
Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
Kumar S., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21359532; PubMed-11466363;
Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S.,
Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- INDUCTION: By INF-alpha and by IFN-gamma in keratinocytes.
                                                                                169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND CHARACTERIZATION.
TISSUE=Epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the interleukin-1 family.";
J. Biol. Chem. 275:10308-10314(2000).
                                                                                PRT;
                                                                                                                                                                                                                                 (1L-1RF2).
ILIF9 OR ILIHI OR ILIE OR ILIRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF200492; AAF69248.1; -. EMBL; AF206696; AAG35670.1; -.
                                                                                                                      28-FEB-2003 (Rel. 41, Created)
                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF206696; AAG
HSSP; P18510; 11TN.
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an
                                                                                HUMAN
                                                                                                                                                                                                                       (IL-1RP2)
                                                                                  I1F9 HUR
Q9NZH8;
                                                               IIF9_HUMAN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Converts 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate into isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.1.2).
1SPH OR LYTB OR BU147.
Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: ISOpentenyl diphosphate + NAD(P)(+) + H(2)O (B)-4-hydroxy-3-methylbut-2-en-1-yl diphosphate + NAD(P)H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome seguence of the endocellular bacterial symbiont of aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      symbiotic bacterium).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF 00191; -; 1.
InterPro; IPR003451; LytB.
Pfam; PF02401; LYTB; 1.
TIGRFAMS; TIGR0216; ispH lytB; 1.
ISOPrene biosynthesis; Complete proteome; Oxidoreductase; NADP.
SEQUENCE 319 AA; 35741 MW; 69DBAFCC12DD09B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 319;
GOOGO CONTRACTOR OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT OF STATEMENT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 169;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         18721 MW; F00A9243706F4154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -! - SIMILARITY: Belongs to the ispH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001118; BAB12865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 70.07
                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 88.9
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buchnera sp. APS.";
Nature 407:81-86(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SELGKSYNT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISPH BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
```

3 SELGKSTNTF 12

à

Genew; HGNC:15741; IL1F9.

qq

```
Query Match
Best Local Similarity
            060858; OBD047; OSCOLL:
16-OCT-2001 (Rel. 40, Created)
16-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ret finger protein 2 (Leukemia associated protein 5) (B-cell chronic lymphocytic leukemia tumor suppressor RFP2) (Tripartite motif protein 13).
RFP2 OR LEUS OR TRIMI3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparative sequence analysis of a region on human chromosome 13q14, frequently deleted in B-cell chronic lymphocytic leukemia, and its homologous region on mouse chromosome 14.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98258969; PubMed=9599022;
Kapanadze B., Kashuba V., Baranova A., Rasool O., van Everdink W.,
Liu Y., Syomov A., Corcoran M., Poltaraus A., Brodyansky V.,
Syomova N., Kazakov A., Ibbotson R., van den Berg A., Gizatullin R.
Fedorova L., Sulimova G., Zelenin A., Deaven L., Lehrach H.,
Grander D., Buys C., Oscier D., Zabarovsky E.R., Einhorn S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kapanadze B., Makeeva N., Corcoran M., Jareborg N., Hammarsund M.,
Baranova A., Zabarovsky E., Vorontsova O., Merup M., Gahrton G.,
Jansson M., Yankovsky N., Binhorn S., Oscier D., Grander D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Migliazza A., Bosch F., Komatsu H., Cayanis E., Martinotti S., Toniato E., Guccione E., Qu X., Chien M., Murty V.V., Gaidano G., Inghirami G., Zhang P., Fischer S., Kalachikov S.M., Russo J., Edelman I., Efetratiadis A., Baral Favera R.; Mucleotide sequence, transcription map, and mutation analysis of 13q14 chromosomal region deleted in B-cell chronic lymphocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A cosmid and cDNA fine physical map of a human chromosome 13q14 region frequently lost in B-cell chronic lymphocytic leukemia and identification of a new putative tumor suppressor gene, LeuS."; FEBS Lett. 426:266-270(1998).
                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
MEDILIBE-21231161; PubMed=11331580;
Reymond A., Meroni G., Fantozzi A., Merla G., Cairo S., Luzi L.,
Riganelli D., Zanaria E., Messali S., Cainarca S., Guffanti A.,
Minucci S., Pelicci P.G., Ballabio A.;
"The tripartite motif family identifies cell compartments.";
EMBO J. 20:2140-2151(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                   407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE=21164809; PubMed=11264177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21100862; PubMed=11161783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics 70:327-334(2000).
                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood 97:2098-2104 (2001)
: [||| | ||
232 AELGKETGTF 241
                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ankovsky N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sangfelt 0.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Lung;
                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pearce A
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Enropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Soares M.B., Bramer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheerz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Arana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzrane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Aranacha M., Madan A., Rodrigues S., Sanchez A., Wollman A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Generation and initial analysis of more than 15,000 full-length Phuman and mouse cDNA sequences."; Purce T. FUNCTION: May act as a tumor suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- DISEASE: May be involved in B-cell chronic lymphocytic leukemia (B-CLL) with a 13q14 region deletion.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 B box-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50119; ZF BBOX; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS50089; ZF RING 2; 1.
Anti-oncogene; Zinc-finger; Coiled coil; Alternative splicing; Polymorphism.
ZN_FING 10 58 RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VSP 005746.
Missing (In isoform Beta).
/FTId=VSP_005747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soId=060858-2; Sequence=VSP_005746, VSP_005747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTIG=VAR_013512.
E3B624345474AEBA_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B BOX-TYPE.
COLLED COIL (POTENTIAL).
L -> D (in isoform Beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=060858-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AJ224819; CAA12136.1; --
EMBL, AF241849; AAKS1624.1; --
EMBL, AF220127; AAF91315.1; --
EMBL, AF220127; AAG53500.1; --
EMBL, AF220128; AAG5550.1; --
EMBL, AL1370660; AAK13059.1; --
EMBL, AL137060; CAC43391.1; --
EMBL, BC003579; AAH03579.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000315; Znf_Bbox.
InterPro; IPR001841; Znf_ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00643; zf-B box; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00336; BBOX; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:9976; RFP2.
MIM; 605661; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
131
200
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
172
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZN FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
```

DB 1; Length 407;

Pred. No. 30;

Score 37;

51.4%;

988 AA

STANDARD;

```
SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   lipoprotein of Erwinia chrysanthemi 3937.";
Mol. Microbiol. 19:455-466(1996).
-!- FUNCTION: PROBBALY INVOLVED IN THE DEGRADATION OF METHYLATED OLIGOGALACTURONIDES PRESENT IN THE PERIPLASM.
-!- CATALYTIC ACTIVITY: Pectin + N H(2)O = N methanol + pectate.
-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF01095; Pectinesterase; 1.
PROSITE; PS00800; PECTINESTERASE 1; 1.
PROSITE; PS00503; PECTINESTERASE 2; 1.
Hydrolase; Aspartyl esterase; Outer membrane; Lipoprotein; Signal;
                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pectinesterase B precursor (EC 3.1.1.11) (Pectin methylesterase B)
                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of pectin methylesterase B, an outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 433; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                          Shevchik V.E., Condemine G., Hugouvieux-Cotte-Pattat N., Robert-Baudouy J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-palmitoyl cysteine.
S-diacylglycerol cysteine.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY.
4854AD25F7619B18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- INDUCTION: By pectin.
-!- SIMILARITY: Belongs to the pectinesterase family.
 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PECTINESTERASE B.
                                                                                                                                    433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 32;
3; Mismatches
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000070; Pectinesterase.
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96228695; PubMed=8830237;
    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X84665; CAA59151.1; -. PIR; S70914; S70914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:: | : || |
192 CATKAGATINITC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46793
                                                            94 CKGHLGQPLNIFC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGKSTNTFC 13
                               1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
    Conservative
                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                        Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=556;
    . 9
                                                                                                                                                                                                                                                                                                                                                STRAIN=3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anchor.
                                                                                                                                    PMEB ERWCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                           (PE B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                    PMEB_ERWCH
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                     g
```

RESULT 12 PCK1_SCHPO

```
MEDLINE=21848401; PubMed=11859360;

RA MEDLINE=21848401; PubMed=11859360;

RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgourco J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgeon G.,

RA Gentles S., Goble A., Hamilin N., Harris D., Hidalgo J., Hodgeon G.,

RA Gentles S., Mungall K., Murphy L., Miblett D., Odell C.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Jones P., Moule S., Mungall K., Murphy L., Miblett D., Odell C.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Allorer K., O'Nell S., Pearson D., Walsh S. V., Warren T., Whitehead S.,

RA Rutherford K., Taylor R.G., Tive R., Squares R., Squares S., Stevens K.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Haylor K., Taylor R.G., Tive R., Robben J., Grymonprez B.,

RA Gabler S., Molckaert G., Aert R., Robben J., Grymonprez B.,

RA Gabler S., Longer L., Beleck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Gotleau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Deminguez A., Revuelta J.L., Jimene S., Sanchez M., Galzon M., Galilardin C., Sanchez M., Botashkin J.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Porsburg S.L.,

Rhaden S., Rhaden M., Pall S., Nurse P.,

Rhaden S., Revuelta J.L., Mander M., Rainhard M., Forsburg S.L.,

Rhaden S., Revuelte J.L., Mander M., Rainhard M., Rainter B.,

Rhaden S., Revuelte J.L., Weller J., Sanchez M.,

Rhaden S., Revuelte J., McCombie W.R., Paulsen I., Potashkin J.,

Rhaden S., Revuelte J., Revuelte J., Sanchez M.,

Rhaden S., Revuelte J., Revuelte J., Sarrell B., Nurse P., Sarron M.,

Rhaden S., Revuelte J., Revuelte J., Sarrell B., Nurse P., Sarron M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
-!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. PKC
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-93259141; PubMed-8491190;
Toda T., Shimanuki M., Yanagida M.;
"Two novel protein kinase C-related genes of fission yeast are
"Sential for cell viability and implicated in cell shape control.";
EMBO J. 12:1987-1995(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Involved in the control of the cell shape. Target
                                   01-UTM-1994 (Rel. 29, Created)
01-CTT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Protein Kinase C-like I (EC 2.7.1.-).
PCKI OR SPAC17G8.14C OR SPAC22H10.01C.
Schizosaccharomyces pombe (Fission yeast).
Elwaryota, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the inhibitor staurosporine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenebB SPombe, SPACI7GB.14c; -..
InterPro, IPR000008; C2.
InterPro, IPR008973; C2 CalB.
InterPro, IPR00873; C2 CalB.
InterPro, IPR00219; DAG PE-bind.
InterPro, IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D14337; BAA03267.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z69730; CAA93602.1; -. Z69795; CAA93697.1; -.
                                                                                                                                                                                                                                                               Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q63450; 1A06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subfamily.
```

```
SMART; SM00139; C1; 2.
SMART; SM00139; C2; 2.
SMART; SM00139; C2; 1.
SMART; SM00131; STK x; 1.
PROSITE; PS00479; DAG PE BIND DOM 1; 2.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
TRANSFERSE; Serine/thronine-protein Kinase; ATP-binding; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
POLY-PRO.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
MW; 26A4ADD42849F37C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHORBOL-ESTER AND
PHORBOL-ESTER AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 87;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB Dred. No. 87;
                                                                                                             InterPro; IPR000015; Prot Kinase.
InterPro; IPR000861; REM_repeat.
InterPro; IPR0008271; Ser_thr_pkin AS.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00180; DAG_PE-bind; 2.
Pfam; PF00185; HR1; 2.
Pfam; PF00185; HR1; 2.
Pfam; PF00433; pkinase; 1.
Pfam; PF00433; pkinase; 1.
                                                                        InterPro; IPR002219; DAG PE-bind.
InterPro; IPR000961; Pkinase C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97321807; PubMed=9178509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            996 CKEEMWYGSTTSTFC 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CASEL--GKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.77
Conservative
7, Conservative
                                                         interPro; IPR008973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phorbol-ester
DOMAIN 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NP BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
YOH5 YEAST
               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=ATCC 48329 / C2;

OBSET B.M., YOGEV OC.;

Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.

-:- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. PKC
                                                                            R Pfam; PF00168; C2; 1.

R Pfam; PF00130; DAG PE-bind; 2.

R Pfam; PF00069; pkinase; 1.

R Pfam; PF000001; Prot_kinase; 1.

R SMART; SM00109; C2; 1.

R SMART; SM00109; C2; 1.

R SMART; SM0013; S TK X; 1.

R SMART; SM0013; B TK X; 1.

R SMART; SM0013; DAG PE BIND DOM 1; 2.

R PROSITE; PS00419; DAG PE BIND DOM 1; 2.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ST; 1.

R PROSITE; PS001109; PROTEIN KINASE ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 530 PHORBOL-ESTER AND DAG BINDING 2.
664 923 PROTEIN KINASE.
670 678 ATP (BY SIMILARITY).
693 4TP (BY SIMILARITY).
789 789 BY SIMILARITY.
789 789 ANUASTKNP -> SNGGFDGES (IN REF. 1)
988 AA; 111783 MW; 0969BDECIAB43C4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cochliobolus heterostrophus (Drechslera maydis).
Bukaryota; Fuydi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHORBOL-ESTER AND DAG BINDING 1.
PHORBOL-ESTER AND DAG BINDING 2.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
InterPro; IPR000719; Prot kinase.
InterPro; IPR00861; REM repeat.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence
16-OCT-2001 (Rel. 40, Last annotation
Protein kinase C-like (EC 2.7.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.4%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || :|:|||
817 LGNTTSTFC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 LGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COCHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT SITE
```

DOMAIN NP BIND BINDING

DOMAIN DOMAIN

SEQUENCE Query Match

Matches

δ 임 KPC1 COC 042632;

ä

Gaps

5.

Indels

DAG BINDING 1. DAG BINDING 2.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
YOH5 YEAST STANDARD; PRT; 1294 AA., 008234; 208234; 208234; 208233; 2008234; 208240 Conversed; 20180041997 (Rel. 35, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Probable ATP-dependent transporter YOL074C/YOL075C. YOL074C/YOL075C. Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycess.
                                                                                                                                                                                                                                                                                     Tzermia M., Katsoulou C., Alexandraki D.;
"Sequence analysis of a 33.2 kb segment from the left arm of yeas
chromosome XV reveals eight known genes and ten new open reading
frames including homologues of ABC transporters, inositol
phosphatases and human expressed sequence tags.";
Yeast 13:583-589(1997).
```

EMBL; Y15839; CAA75801.1; -. PIR; T43051; T43051.

```
-
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=902659039; PubMed=2161319;
MEDLINE=902659039; PubMed=2161319;
Horen M.S., Bankier A.T., Beck S., Bobni R., Brown C.M., Cerny R.,
Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A.,
Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.,
"Analysis of the protein-coding content of the sequence of human
cytomegalovirus strain AD165.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                          PROSITE; PS00211; ABC TRANSPORTER 1; 2.
PROSITE; PS50893; ABC TRANSPORTER 2; 2.
Hypothetical protein; ATP-binding; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C555500A45E9284E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; deDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
ATP (POTENTIAL).
ATP (POTENTIAL).
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
                                                                                                       EMBL; 274817; CAA99085.1; -.
EMBL; 274816; CAA99084.1; -.
PIR; 877690; 877690.
GermChline; 143497; -.
SGD; S0005435; YOLO75C.
INTERPRO; IPR003593; AAA_ATPase.
InterPro; IPR003139; ABC_transporter.
Pfam; PF00005; ABC_tran; 2.
ProDom; PD000066; ABC_transporter; 2.
SWART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus (strain AD169).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1294 AA; 145157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1161 CGERLGIMTNTF 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein UL16. UL16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 58.3.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   528
983
1062
                                                                                                                                                                                                                                                                                                                                                                                             Transport; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UL16 HCMVA
P16757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
NP_BIND
NP_BIND
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
UL16 HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC DT AAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FOTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ..)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36.5; DE
Pred. No. 20;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5, 2004, 09:56:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X17403; CRA3548.1; -. PIR; S09778; S09778. Hypothetical protein. CARBOHYD 35 35 N-CARBOHYD 68 68 N-CARBOHYD 68 68 N-CARBOHYD 95 N-CARBOHYD 101 101 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD 132 N-CARBOHYD N-CARBOHYD 132 N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARBOHYD N-CARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26147 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 5/....
Best Local Similarity 5/....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CASELG-KSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: September
Job time: 7.90909 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
68
84
95
101
132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41
68
84
95
101
132
145
230 AA;
```

```
Query Match
70.8%; Score 51; DB 11; Length 326;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SW00141; PDGF; 1.
PROSITE; PS00249; PDGF=1; 1.
PROSITE; PS50278; PDGF=2; 1.
SEQUENCE 326 AA; 37\overline{1}{1}06 MW; D7CAEBA6C9FABB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q918V8 rana pipien
Q810x5 rana pipien
Q80x51 trypanosoma
Q9544 pneumocysti
Q90zb2 brachydanio
Q10xb2 paramecium
Q81j8 bacillus an
Q81j8 bacillus an
Q81j8 bacillus ac
Q7yyt2 cryptospori
Q94k1 arabidopsis
Q9fk1 arabidopsis
Q9fk1 arabidopsis
Q91133 arabidopsis
Q9m133 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91ze4 rattus norv
                                                                                                                                                                                         5, 2004, 09:46:09; Search time 29.4141 Seconds (without alignments) 139.448 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91ZE4
Q8UVX
Q8UVX
Q9547Z1
Q95244
Q90ZE2
Q7UWW5
Q84551
Q814IQ
Q914IQ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q97YYHZ
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPTREMBL_25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_tung:*
4: sp_tung:*
5: sp_tung:*
5: sp_tung:*
6: sp_tunge:*
7: sp_manmal:*
7: sp_mhc:*
7: sp_mhc:*
7: sp_organelle:*
7: sp_organelle:*
7: sp_organelle:*
7: sp_organelle:*
7: sp_organelle:*
7: sp_organelle:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unclassified: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_rvirus:*
sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                   1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp plant: *
sp rodent: *
sp virus: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_archeap:*
                                                                                                                                                                                                                                                                                                                          US-09-761-636A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
110
110
110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326
127
127
1011
316
283
383
605
605
621
128
471
738
                                                                                                                                                                                             September
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 556.9
557.6
557.6
557.6
557.6
557.6
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
557.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11:
22:
23:
14:
12:
14:
15:
16:
16:
                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.440
39.55
39.55
39.99
39.99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š.
```

Q8iiz5 plasmodium Q9r4a0 lactobacill Q9r499 lactobacill Q9up2 pneumocysti Q9dfy8 rana catesb Q8498 human immun Q9yxm6 human immun Q9yxm6 human immun Q9yxm7104 pneumocysti Q9s312 prochloroco Q81tv5 bacillus an Q76115 human immun Q76115 human immun	Q76104 human immun Q76107 human immun Q7608B human immun Q7609B human immun Q76106 human immun Q76106 human immun Q76108 human immun Q76083 human immun Q76081 human immun Q76109 human immun Q76110 human immun Q76110 human immun Q76110 human immun Q76114 human immun Q76114 human immun Q76114 human immun Q76114 human immun Q76114 human immun	ALIGNMENTS  PRT; 326 AA.  reated)  ist sequence update)  ist annotation update)  Craniata; Vertebrata; Euteleostomi;  Sciurognathi; Muridae; Murinae; Rattus.	nan J., Steffen A., Waltenberger J., a J.P.; s which specifically inhibit VEGF-C-and 3FR-3 but not VEGFR-2."; activity; IEA. activity; IEA. if. cactivity.
15 13 13 13 13	1104 1106 1106 1106 1108 1108 1109 1109 1110 1110 1114	ALIGNMENTS RT; 326 ated) t sequence t annotati raniata; V	an J., Sl. J.P.; which sp. FR-3 but activity d/or mail t. actor.
QBIIZS Q9R4A0 Q9R499 Q9UWP2 Q9DFYK Q9YXMG O89503 Q9S332 Q9S332 Q9S332 Q9S332 Q9S11V6	Q76104 Q760107 Q760107 Q76098 Q76094 Q76080 Q76080 Q76100 Q76116 Q76101 Q761114	ALIGN PRT; Created) Last sec Last ann; Crania	Krishnan J leeman J.P inones whi of VEGFR-3 1). i i TEA. actor acti: wth and/or repeat. owth_facto:
5 113 115 115 116 116 115	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	19, ( 19, 1 19, 1 19, 1 10, 1 10, 1	Kri Slee Dlinc D01). 11; 1e; 1 Fact Cowth Cowth
21 182 283 283 284 285 286 286 286 334 8334 8334	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ARY; eel. eel. eel. Chor	ey;  s A.,  t ind  ratio  -o(8)  96008  96008  cowth  cowth  11 gi
v. <del>a.</del> a. a. a. a. a. a. a. a. a. a. a. a.		IM) MBI MBI MBI S (	A. Dawle sawle saw
4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	88888888888888888888888888888888888888	- 91 <u>2</u> 40	OM N Jue-I Jazitt Gii Gii Gized Gized 220; 728; 728; 728; 728; 728; 728; 728; 728
<b>െ ഒ ഒ ഒ ഒ മ മ മ മ മ മ മ മ മ</b> മ മ മ മ മ മ		t; -2001 7-2001 7-2003 7-2003 7-2003 7-2003 1-101 1-101 1-101	=Sprag    V.,     V.,     V.,     V.,     M. V.,    -induc  -
1118 119 120 120 120 120 120 120 120 120 120 120	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ULT 1  ZE4  Q91ZE4  Q91ZE4; Q1-ZE4; Q1-DEC-2001 (TrEMBLX 01-UNN-2003 (TrEMBLX VEGP-D. Rattus norvegicus (R Eukaryota; Merazoa; Mammalia; Eutheria; NCBI_TaxID=10116;	SEQUENCE FROM N.A. SIRAIN-Sprague-Dawley; Kirkin V., Mazitschek R., Krishnan J Repper M.S., Giannis A., Sleeman J.P Pepper M.S., Giannis A., Sleeman J.P "Characterization of indolinones whi. VEGF-D-induced activation of VEGFR-3 Eur. J. Biochem. 0:0-0(2001). EMBL; AY032728; AAK66008.1; GO; GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:0008083; F:growth factor activation of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
		RESULT Q91 ZE4 1D Q9 D7 Q9 D7 Q1 D7	

ö

Gaps

· 0

0

Gaps

.. 0

Q918V8;

**0918V8** 

RESULT 2 Q918V8

```
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MITEL. 2;
Bell J.S., Harvey T.I., Sims A.M., Barry J.D., McCulloch R.;
Bell J.S., Harvey T.I., Sims A.M., Barry J.D., McCulloch R.;
Bell J.S., Harvey T.I., Sims A.M., Barry J.D., McCulloch R.;
bell J.S., Harvey T.I., Sims A.M., Barry J.D., McCulloch R.;
submitted for Trypanosoma brucei.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR350880; AAK51796.1;
GO, GO:0005584; F:ATP binding; IEA.
GO, GO:0005284; F:ATP binding; IEA.
GO, GO:0005298; P:Mismatch repair; IEA.
                                                                                                                                                               Score 43; DB 13; Length 127;
Pred. No. 3.5;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR0016432; MutS C.
InterPro; IPR001695; MutS C.
InterPro; IPR001695; MutS III.
InterPro; IPR00189; MutS III.
IPR00189; IPR00189; III.
IPR00189; IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; III.
IPR00189; II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%; Score 43; DB 5; Length 997; 58.3%; Pred. No. 30;
                                                                                                953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative mismatch repair protein MSH8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          997 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                      POTENTIAL
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A.
MEDLINE=20184731; PubMed=10721706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muris.
                                                                      23 PC
14469 MW;
                                                                                                                                                                           59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2003 (TrEMBLrel. 25, Kexin-like protease KEX1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pneumocystis carinii f. sp.
                                                                                                                                                                                                                                                                                                                                                                        98 CKYKLKKSTNKFC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.5.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           460 CGSKRGRTTNTF 471
                                                                                                                                                                                                                                                                                                                        1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CASELGKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma brucei.
                                                                                                        127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pneumocystis.
NCBI_TaxID=42066;
                                                                                                           SEQUENCE
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9P944;
                                        Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9P944
                                                                              SIGNAL
                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9P944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOOR DEAD TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                  g
           S F S
                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABDLINE=20330357; PubMed=10871370;
Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 3' UTR of unusual length and structure.";
Nucleic Acids Res. 28:2375-2382(2000).
BMBL, APIG513; AAF76935.1; -.
BMBL, A99035; A39035.
HSSP; P22069; LONC.
GO; GO:0003876; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
01-0CT-3003 (TrEMBLrel. 25, Last annotation update)
0nconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.1%; Score 49; DB 13; Length 127; 69.2%; Pred. No. 0.26; ive 1; Mismatches 3; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 23 POTENTIAL.
127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AA
                                                                                                                                                                                                                               127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000535; RNSseA; 1.
SMART; SM00092; RNASe PC; 1.
PROSITE; PS00127; RNASE PANCKEATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :| |||||||
98 CKYKLKKSTNTFC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                  126 ASELGKTTNTF 136
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00074; rnaseA;
ProDom; PD000535; RNas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onconase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
```

SIGNAL

Matches

δ 셤 6

Gaps

0

2; Indels

Q8UVX5;

QBUVXS

```
2 ASELGKSTNTFC 13
                                           63 ASFAGRLINTFC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A231L protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain 1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q84551
Q84551;
                                                                                                                                                                      Q7UWW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                Q7UWW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  084551
                                                    q
                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Lee L.H., Gigliotti F., Wright T.W., Simpson-Haidaris P.J.,
Weinberg G.A., Haidaris C.G.,
"Molecular characterization of KEX1, a kexin-like protease in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii; Neopterygii, Teleostei; Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.3%; Score 42; DB 3; Length 1011; 53.8%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.9%; Score 41; DB 13; Length 316; 66.7%; Pred. No. 22; 3; Indels ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112021 MW; FBE472C8F65864E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Gbx2 but not gbx1 is dependent on fgf8 function.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; AF288763; AAK83070.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMARI; Smulles; Low,
PROSITE; PS00021; HOMEOBOX 1; 1.
PROSITE; PS0071; HOMEOBOX 2; 1.
DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Transcription factor Gbx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 AA
                                                                                      Gene 242:141-150(2000).
-!- SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN.
EMBL; AF093132; AAF32493.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 48;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00723; SUBTILISIN.
ProDom; PD000717; P domain; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01483; P_proprotein; 1.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 CAGEIVAAKNIFC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 53.8
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                    Pneumocystis carinii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00389; HOX; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1011 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
2902B2
AC 0902B1
DT 01-DI
DT 01-DI
DT 01-DI
DT 01-DI
DE GRAI
OS Bracl
OC FURE
OC CYPT
ON (1)
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BLUN
RR BRUN
DR RR GO;
DR PROS
RW BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BRUN
RR BR
    RA
RAT
RET
RET
CCC
CCC
CCC
DR
DR
DR
DR
DR
DR
DR
SQ
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

ö

Gaps

. 0

Conservative

Best Local Similarity Matches 8; Conserv

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20013326; PubMed=10544099;
Kaiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing W., Lisec A.D., Nickerson K.W., Van Etten J.L.;
"Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=96.87795; PubMed=8614977;
Lu Z., Li Y., Que Q., Kutish G.F., Rock D.L., Van Etten J.L.;
"Analysis of 94 kb of the chlorella virus PBCV-1 330-kb genome: map positions 88 to 182.";
Virology 216:102-123(1996).
                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of the marine planctomycete Pirellula sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus.
NCBL_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                        Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                              Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.6%; Score 40; DB 16; Length 283; 58.3%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BX294135, CAD72247.1;
Hypothetical protein; Complete proteome.
SEQUENCE 283 AA; 31166 MW; 82926CDCODF3A51A CRC64;
            QTUWNS;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003)
  283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
  PRT;
                                                                                                                                                                                                                                                                                     MEDLINE=22735913; PubMed=12835416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 263:254-262(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 AAELGLSINSYC 220
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                          Rhodopirellula baltica.
```

ö

```
InterPro, IPR001567; Peptidase M3.
InterPro, IPR006025; Pept M Zn_BS.
Pfam; PF01432; Peptidase_M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                  2 ASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F-box domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
7; Conserve
                                                                                              Complete proteome. SEQUENCE 605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7YYH2
Q7YYH2;
                                                                                                                                                                                                                                                                                                                                                                                                                               081410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7YYH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOCOS ON THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPOR
                                                                                                                                                                                                                                                                                                g
           SKRRRR
                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22608414; PubMed=12721629; Read T.D., Peuclean I.T., Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tetrelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Baren A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Xoehler T.M., Hanna P.C., Kolsto A.-B., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.6%; Score 40; DB 12; Length 383; 46.2%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; U42580; AAC96599.1; -.
PIR; T17722; T17722.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Graves M.V., Van Etten J.L.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                   Graves M.V., Van Etten J.L.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 AA; 43643 MW; B04E602D99973DCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0004222; F:metalloendopeptidase activity; IEA. GO:0008270; F:zinc ion binding; IEA. GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus anthracis (strain Ames).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligoendopeptidase F, putative. BAS706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 423:81-86(2003).
EMBL; AE017041; AAP29338.1; -.
TIGR; BA5706; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVMNIGKKKNEFC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.2
Matches 6; Conservative
                                  Virology 276:27-36(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                       Van Etten J.L.;
Submitted (DEC-1995)
                                                                                                                                                                                                                                                                                     Van Etten J.L.;
Submitted (SEP-1997)
                                                                                                                                                                                                                  Submitted (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=198094,
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                               Van Etten J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  081778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
:`
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22608415; PubMed=12721630; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Ivanova N., Sorokin A., Anderson I., Galleron N., Lapidus A., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman B., Larsen N., D'Souza M., Walunas T., Orechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overboek R., Kyrpides N., "Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 605;
                                                     Score 40; DB 16; Length 605;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus anthracis.";

Nature 423:87-91(2003).

ReMBL, ABC17015; AAA12314.1; -...

GO; GO:0016797; F:hydrolase activity; IEA.

GO; GO:0004222; F:metalloendopeptidase activity; IEA.

GO; GO:0006209; F:netalloendopeptidase activity; IEA.

GO; GO:0006508; F:zinc ion binding; IEA.

GO; GO:0005508; P:proteolysis and peptidolysis; IEA.

RINE-Pro; IPR006025; Pepti M. Zn. BS.

Refan; PF01432; Peptidase M3; 1.

Refan; PF01432; Peptidase M3; 1.

Refan; PF01432; Proteome.

Refan; PG01432; Proteome.

Regource 605 AA; 69123 MW; 3C16DB0B1B2F4062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cryptosporidium parvum.
Eukaryota, Alveolata; Apicomplexa; Coccidia; Bimeriida;
Cryptosporidiidae; Cryptosporidium.
NCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=226900;
605 AA; 69285 MW; 138E401597519248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01igoendopeptidase F (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.6%; Score 40; DB 16;
58.3%; Pred. No. 67;
ive 1; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     621 AA
                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                          58.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 ADNVGKSTGAFC 369
                                    Query Match
Best Local Similarity 58.3.
Conservative
7,
                                                                                                                                                                                                                        358 ADNVGKSTGAFC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
```

ö

```
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                        SEQUENCE FROM N.A
                                                                                             STRAIN=Columbia;
                                 NCBI_TaxID=3702;
                                                                                                                                                       Tabata S.;
                                                                                                                                                                                                                  clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FLD9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FLD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8L838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
Q9FLD9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                      Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
"Integrated mapping, chromosomal sequencing and sequence analysis of Cryptosporidium parvum.";
Genome Res. 0:0-0(2003).
EMBL; BX538351; CAD98511.1;
SEQUENCE 621 AA; 71995 MW; D99793733B5A3658 CRC64;
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Genomic DNA, chromosome 5, Pl clone:MAB16.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-OCT-2003 (TrEMBLrel. 25, Last annotate)
1-OCT-2003 (TrEMBLrel. 26, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                            Length 621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 13; Length 128;
Pred. No. 21;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RC-RNASE3 RIBONUCLEASE.
2B14986082E0587D CRC64;
                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA.
                                                                                                                                                                                                                    54.9%; Score 39.5; D
56.2%; Pred. No. 86;
tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  471 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodom; PD000535; RNASEA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF242554; AAG31440.2; -. HSSP; P22069; 10NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 23 PK
24 128 Rt
128 AA; 14517 MW;
                                                                                                                                                                                                                                                                                                                            161 CASESTFEGERQNTFC 176
                                                                                                                                                                                                       Query Match
Best Local Similarity 56.2%;
                                                                                                                                                                                                                                                                                                   1 CASEL --- GKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 CHYKLSSSTNTIC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8400;
                                       STRAIN=Iowa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                            O9DFY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9FHK1
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
Q9DFY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
Db
                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC DIT DIT OCC OCC OCC OCC
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids,
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 5. IV. Sequence features of the regions of 1,456,315 bp covered by nineteen physically assigned Pl and TAC clones.";

DNA Res. 5:41-54(1998).

EMBL; AB010077; BAB10221.1; -.

SEQUENCE 677 AA; 74196 MW; POC2B09B86E1B079 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequer
features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
Tabata S.;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 10; Length 67
Pred. No. 1.2e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                            55212 MW; 1E5D997B7942E26C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
51milarity to hedgehog-interacting protein.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBL838;
01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 1
Pred. No. 80;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738 A.A.
                                                                                                                                                                                                         InterPro; IPRO01810; F-box.
InterPro; IPR006527; F-box.
InterPro; IPR006527; F-box. assoc_1.
Pfan; PF00646; F-box; 1.
SWART; SW00256; FBOX; 1.
TIGRPAMS; TIGR01640; F-box.assoc_1; 1.
FROSITE: PS50181; FBOX; 1.
SEQUENCE 471 AA, 55212 WW; IE5D997B75
                                                                                                                                      DNA Res. 7:31-63(2000).
EMBL; AB018112; BAB10975.1; -.
EMBL; AB026661; BAB10975.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Columbia;
MEDLINE-98290546; PubMed=9628582;
                                                                                                                                                                                                                                                                                                                                                                                                                            54.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.2%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 DLGESTNKYC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 SEIWKSSNDFC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 SELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
Q8L838
ID Q8L833
AC Q8L831
DT 01-OC'DT
```

```
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M.,
Palm C.J., Bowser L., Jones T., Bahh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narnsaka M., Pham P.K., Sakano H.,
Ecker J., Theologis A., Davis R.W.;
Submirted (UTN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY120763; AAM53321.1; -
Hypothetical protein.
SEQUENCE 738 AA; 82977 MW; RF9BIB0FDA7BISCE CRC64;
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
AT4G01400.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 58.3%; Pred. No. 1.38+02;
Matches 7; Conservative 3; Mismatches 2; Indels
```

Search completed: September 5, 2004, 09:59:52 Job time : 31.4141 secs

1 CASELGKSTNTF 12

à q

. 0

0; Gaps

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

using sw model - protein search, OM protein

09:37:49 ; Search time 42.6768 Seconds (without alignments) 86.068 Million cell updates/sec 5, 2004, September Run on:

CASELGKSTNTFC 13 US-09-761-636A-5 score: Sequence: Perfect

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A Geneseq 290an04:*

1: geneseqp1980s:*

3: geneseqp200s:*

4: geneseqp2001s:*

5: geneseqp2003s:*

6: geneseqp2003ss:*

7: geneseqp2003bs:*

8: geneseqp2004ss:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Aau04524 VEGF base	VEGF	VEGF	VEGF	VEGF	5 VEGF	7 VEGF	Aau04547 VEGF base	1 VEGF	9 VEGF	6 VEGF	Aau04548 VEGF base	Human	0 Human	Human	Human	Abb84621 Human wil			Homo s	Aav97572 Human VEG	Human	Human		Aab10649 Hilman VEG
SUMMAKIES	ID	AAU04524	AAU04527	AAU04534	AAU04550	AAU04546	AAU04535	AAU04537	AAU04547	AAU04551	AAU04549	AAU04536	AAU04548	AAU04522	AAU04520	AAY23889	AAB11931	ABB84621	ABG73750	ABG73779	AAW53240	AAY97572	AAW44293	AAW49036	AAW53241	AAB10649
	DB	4	4	4	4	47	4	4	4	4	4	4	4	4	4	~	m	ø	9	9	7	4	7	~	N	٣
	Length	13	17	13	17	17	13	13	17	17	17	13	17	73	96	109	109	109	109	287	325	325	354	354	S	354
₩	Query Match	100.0	100.0	95.8	95.8	95.8	90.3	90.3	90.3	90.3	90.3	84.7	84.7	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0
	Score	72	72	69	69	69	65	65	65	65	65	19	61	54	54	54	54	54	54	54	54	54	54	54	54	54
	Result No.	-	7	m	4	ហ	9	7	œ	ወ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aay70750 Human pre	Human	Human	Aab37606 Human VEG	Aab70685 Human vas	Aay97573 Human VEG	Aau08441 Polypepti	Abq33055 Human vas	Human	Human		Aaw14994 Human C-F	Aam47933 Mouse VEG	Aay08287 Human gro		Aam47931 Mouse VEG	Aaw44296 Rat vascu	Aay08286 Human gro		Aaw44295 Mouse vas
AAY70750	AAY70983	AAB29049	AAB37606	AAB70685	AAY97573	AAU08441	ABG33055	ABG32046	ABB84623	ADD08950	AAW14994	AAM47933	AAY08287	AAW53243	AAM47931	AAW44296	AAY08286	AAW14992	AAW44295
m	m	m	4	4	4	4	Ŋ	Ŋ	9	۲	~	'n	~	7	S	~	0	N	7
354	354	354	354	354	354	354	354	354	354	354	620	110	178	321	321	326	337	358	358
75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0		70.8	-	9.04		70.8	70.8	70.8
5.4 4.	54	54	54	54	54	54	54	54	54	54	54	21	21	21	51	21	21	21	21
26	27	28	59	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

## ALIGNMENTS

AAU04524 standard; peptide; 13 AA. VEGF based monocyclic peptide 1. (first entry) 26-SEP-2001 AAU04524; RESULT 1
AAU04524
ID AAU0
XX
AAU AAU
XX
DT 26-6
XX
XX
HUM
KW HUM
KW HOIS
XX
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW HIM
KW KW HIM
KW KW HIM
KW KW HIM
KW KW HIM
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW KW LG
KW K

Human: VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

1. .13 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Stacker S, Hughes RA, WPI; 2001-442248/47. Achen MG,

Cendron A;

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

```
peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, consistent or Imphanojogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphanojogenesis, arthropathy, creterised by angiogenesis, neovascularisation or lymphanojogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, creterised by angiogenesis, neovascularisation of the liver, excessive creebrovascular accident, post-angioplasty restenosis, head, heat or clamma, substance-induced neovascularisation of the liver, excessive cremens, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF vEGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide, to to residue 10 f the sequence appearing as AAU04528, also forming a dimeric peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy, chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 72; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels

    .13
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGF based bicyclic dimeric peptide #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04527 standard; protein; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Achen MG, Hughes RA, Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
```

```
The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human conversed (ascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betaction distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptides (loop fragment from an exposed loop of a growth factor protein and cyclising the peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis,

The condition is diabeted retinopathy, psoriasing, arthropathy, characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabeter retinopathy, psoriasing, arthropathy, carebrovascular accident, post-angioplasty restenosis, head, heat or cold crauma, substance-induced neovascular sequelae, host of the liver, excessive conference in fection. The peptides are also used to modular vascular permeability in a mammal the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or by any and proved to interfere and interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or by interference or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
                                               Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF. Or F.O and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 72; DB 4; Length 17; 100.0%; Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels

    13
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04534 standard; peptide; 13 AA.
                                                                                                                                                                                        Claim 59; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEGF based monocyclic peptide 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200152875-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU04534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU04534
     %XGLGCCCCCCCCCCCCCCCCCXXXXAAAAXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
The sequence represents a monometric monocyclic peptide or the invention, whose 3-dimensional structure is modelled on the expose loop of human beta carbon definition whose 1-dimensional structure is modelled on the expose loop of human beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide by oxidising the periode by oxidising the monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis. The monocyclic peptides and a cyclic peptides with a least one amino acid deleted prior cyclisation are used to interfere with angiogenesis.

CC ovalisation are used to interfere with angiogenesis.

CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.

CC crebrovascular accident, post-angioplasty restenosis, head, heat or cold creama substance-induced neovascularisation of the liver, excessive creame, substance-induced neovascularisation of the liver, excessive confection. The peptides are also used to modulate vascular permeability accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or branding and peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VECF. Cor-D and corruct inflammation, especially rheumatoid arthritis, psoriasis and disheric retrinomathy.
                                                                                                                                                                                                                                                                                 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                                                                                                                                                                                                                                                         Example 25; Page 47; 102pp; English.
                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
  18-JAN-2001; 2001WO-US001533.
                                                18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                Hughes RA,
                                                                                                                                                                                                                                WPI; 2001-442248/47.
                                                                                                                                                                              Achen MG,
                                                                                                                                                                                                                                                                                                                                                              residues.
```

Sequence 13 AA;

```
Gaps
                                .;
0
Score 69; DB 4; Length L., Pred. No. 6.8e-05;
                             1; Mismatches
         95.8%;
                 92.3%;
                            12; Conservative
                  Local Similarity
         Query Match
                            Matches
```

·,

à

AAU04550 standard; peptide; 17 AA.

VEGF based bicyclic dimeric peptide #7.

RESULT 4
AAU04550
ID AAU04550
XX
XX
XX
DDT 26-S
XX
KW Huma
KW Huma
KW diab
KW diab
KW Giab
KW Synt
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW Giab
KW

(first entry) 26-SEP-2001 AAU04550;

Human; VEGF; vascular endothelial growth factor; angiogenesis;

neovascularisation, lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Synthetic

/note= "A disulfide bond forms between residue 17 and residue 1 of the sequence appearing as AAU04528, forming a dimeric peptide" .13 /note= "This bond cyclises the peptide" Location/Qualifiers Disulfide-bond Disulfide-bond 

WO200152875-A1

Cendron A;

Stacker S,

18-JAN-2001; 2001WO-US001533

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Stacker S, Hughes RA, Achen MG,

Cendron A;

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine WPI; 2001-442248/47.

Example 26; Page 49; 102pp; English.

residues.

The Sequence represents a cumeric Discrete periods of human whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human consists of periods of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a cyclising the peptide by oxidising the eysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with anglogenesis. The monocyclic peptides dimeric bicyclic peptides in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, heat or crebrovascular accident, post-angloplasty restenosis, heat or crebrovascular substance-induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver crauma, substance-induced neovascular sequelae, or chronic liver crauma, substance-induced neovascular sequelae, or chronic liver craumal has a condition of the liver, pleura, cin a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lumgs, peritoneal cavity, cor brain The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfece cutth at least one biological activity induced by VEGF or D and chabetic retinopathy certain with an anti-inflammatory agent, to treat a chronic inflammation with an anti-inflammatory agent, to treat a channel of the peptides are used continual and and activity induced by VEGF or D and dabbetic retinopathy. The sequence represents a dimeric bicyclic peptide of the invention, diabetic retinopathy

Sequence 17 AA;

Length 17; Score 69; DB 4; Length 17; Pred. No. 9.1e-05; L; Mismatches 0; Indels 95.8%; Conservative Query Match Best Local Similarity

. 0

Gape

; 0

1 CASELGKSTNTYC 13 g

1 CASELGKSTNTFC 13

ò

AAU04546 standard; peptide; 17 AA. AAU04546 ID AAU0

셤 à

```
Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "A disulfide bond forms between residue 17 and residue 17 of an identical peptide to form a dimeric peptide."
                                                                                                                                                                      vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                            neovascularisation, lymphangiogenesis, psoriasis; tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cendron A;
                                                                                                          VEGF based bicyclic dimeric peptide #3.
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 1. .13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2001; 2001WO-US001533
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200152875-A1
                                                      26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2001
                                                                                                                                                                                                                                                                                                                     Synthetic.
AAU04546;
```

The sequence represents a dimeric bicyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betace carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and conclusing the by oxidising the peptide by oxidising the monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclication are used to interfere with angiogenesis.

CC peptides) and a cyclic peptide with at least one amino acid deleted prior conclusion are used to interfere with angiogenesis.

CC peptides by angiogenesis, neovascularisation or lymphangiogenesis.

CC crecondition is diabetic retinopathy, psoriasis, arthropathy, carebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive cordification in peripheral limps or in lungs, peritoneal cavity, pleura, or brain. The peptides are also used to modulate vascular permeability in a communation in peripheral limps or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vesels and lymphatic contendiation. The peptides are used to image blood vesels and lymphatic contendiation in peripheral limps or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vesels and lymphatic contendiation and bicyclic peptides are used to interfere contendiation enterpretation with an anti-inflammatory agent, to treat a cordinal criminal activity induced by VEGF, VEGF, cordination enterpretation and proposition are also used in combination with an anti-inflammatory agent, to treat a characterized by activates and advanced to retrain and activation and archivation and activation archivation and activation and activation archiv diabetic retinopathy

Example 26; Page 49; 102pp; English.

residues.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-composed to a growth factor protein and peptide loop fragment from an exposed loop of a growth factor protein and composition the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior composition are used to interfere with angiogenesis, concuracterised by angiogenesis, neavascularisation or lymphangiogenesis in a mammal with a condition is diabetic retinopathy, psoriasis, arthropathy, contracterised by angiogenesis, neavascularisation or lymphangiogenesis and condition is diabetic retinopathy, psoriasis, arthropathy, contracterised manacolatic neovascularisation of the liver, excessive trauma, substance-induced neovascularisation of the liver, excessive commone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid

Sequence 17 AA;

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                          Gaps
                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                     Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
Length 17;
        9.1e-05;
8.1e-05;
% 0; Indels

    13
/note= "This bond cyclises the peptide"

  Score 69; DB 4;
Pred. No. 9.1e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cendron A;
                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacker S,
                                                                                                                                                                                                                                     AAU04535 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                 VEGF based monocyclic peptide 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
    95.8%;
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                CATELGKSTNTFC 13
                                                                                      1 CASELGKSTNTFC 13
                          Best Local Similarity 92.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200152875-A1.
                                                                                                                                                                                                                                                                                                                            26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                  AAU04535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues
        Query Match
                                                                                                                                                                                                RESULT 6
```